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version 4.5 - 2000 Compugen

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Result
No.
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Database
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Title:
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                                                                                                                                                                                                 Score
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                                                                                                                                                                                                                                                                          No. 1s the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution.
 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           length:
1000.0
                                                                                                                                                                                                 Match
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Maximum Match 100%
Listing first 45 summaries
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127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            522463 seqs,
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/SIDS8/gcgdata/geneseq/geneseqp/AA1981.DAT:
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/SIDS8/gcgdata/geneseq/geneseqp/AA19
/SIDS8/gcgdata/geneseq/geneseqp/AA19
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/SIDS8/gcgdata/geneseq/geneseqp/AA1984.DAT:*
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                                                                                                                                                                                                                                                                                                                                          /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*
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/SIDS8/gcgdata/geneseq/geneseqp/AA1994.DAT:*
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                                                                                                                                                                                                 Length
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/gcgdata/geneseq/geneseqp/AA1992.DAT:*
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AAP60416
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                                                                                                             AAY70282
AAR66442
AAR13175
AAR07945
               AAP83144
                                                 AAR13178
AAR13179
                                                                                AAR13176
AAR13177
                                                                                                                                                                                                                                               SUMMARIES
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5.481 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /AA1985.DAT:*
/AA1986.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             'AA1982.DAT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             522463
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           87 .DAT: *
Sequence
CS protei
           Plasmodium falcipa
Plasmodium falcipa
NS1_81-RLfdelta9
NS181RLFAuth plasm
NS1_81-RLfAuth + (
NS1_81-RLfAuth + (
NS1_81(NANP)4RLfAu
NS1_81(NANP)4RLfAu
NS1_81(NANP)4RLfAu
Recombinant Vaccin
Sequence encoded b
                                                                                                                                                                                               Description
protein
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um falc	AAB98457		21	41.7	53	٠.
1	AAB84447	22	21	41.7	53	_
fal	AAG89366	22		41.7		w
falc	26	22	21	41.7		~
fa	AAG84517	22		41.7	53	
fa	AAG62428	22	21	41.7		_
- in	970	22	21	41.7		Ψ
1f1ed	AAY58777	21	21	41.7	53	w
	AAY54553		21	41.7		_
Pathogen derived T	AAY80071	21	21	41.7		٠,
ved f	AAY23252	20	21	41.7		٠.
T-cell stimulatory	AAW35440	18	21	41.7	53	_
7	AAW05612	17		41.7		w
a circumspo	AAR70912	16	21	41.7	53	.~
đ	AAR75955	16	21	41.7	53	
a cir	AAR78920	16	21	41.7	53	_
3	AAR82586	16		41.7	53	٣
Sequence of modifi	AAP91504	10	21	41.7	53	w
m CS p	AAJ04118	22	20	41.7	53	7
þ	AAY99033	21	19	41.7	53	٠,
Human IL-2/ P. yoe	AAB07288	21	478	44.5	σ.	٠,
Plasmodium berghei	AAP93560	10	272	46.1	8	-
Circumsporozoite a	AAR07291	1	168	46.1	58.5	~
CS Region II+ mime	AAR71654	σ		46.1		~
Plasmodium cynomol	AAP70709	œ		7.		_
Sequence corresp.	AAP61002		19	48.8		_
Circumsporozoite a	AAR71655	σ	14	в.	62	ŭ
Plasmodium falcipa	œ	21	21	5٠		~
CS Region II+ mime	AAR71651	16		59.1	75	•
P.falciparum deriv	AAR87213	16		5	96	٠.
유	AAR07290	H	180	94.5	120	٠.
RTS* protein. Syn	AAR37797	14	424	95.3	121	
ence encoded	AAP80835	9	412		123	_
RTS protein. Synt	AAR37796	14	424	100.0		

ALIGNMENTS

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RESULT
AAY70282
  Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; T-cell epitope; tetanus toxold; antigenic epitope; treatment circumsporozoite protein; CSP; sporozoite surface protein-1; liver stage antigen-1; LSA-1; merozoite surface protein-1; M
                                                                                                                                                                                                       apical membrane antigen-1; A
EBA-175; rhoptry associated
                                                                                                                                                                                                                                                                                      Plasmodium falciparum CSP antigenic epitope, P593
                                                                                                                                                                                                                                                                                                             06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                         AAY70282 standard; peptide;
WPI; 2000-237654/20
                      Lal AA,
                                                                               21-AUG-1998;
                                                                                                      19-AUG-1999;
                                                                                                                           02-MAR-2000.
                                                                                                                                                 WO200011179-A1
                                                                                                                                                                        Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                   AAY70282;
                                                                                                                                                                                             Pfg27; antiparasitic;
                                            (USSH)
                                                        (NAIM-)
                                            NAT INST IMMUNOLOGY.
US DEPT HEALTH & HUMAN SERVICES
                      Shi YP,
                                                                                                                                                                                                                                                                                                            (first entry)
                                                                               9805-0097703.
                                                                                                      99WO-US18869
                     Hasnain SE;
                                                                                                                                                                                               prevention;
                                                                                                                                                                                                                     AMA-1;
                                                                                                                                                                                                                                                                                                                                                           23
                                                                                                                                                                                                            protein-
                                                                                                                                                                                                                                                                                                                                                           3
                                                                                                                                                                                               anti-CDC/NIIMALVAC-1
                                                                                                                                                                                                                                                      malaria; vaccine;
treatment;
                                                                                                                                                                                                         specific antigen;
                                                                                                                                                                                                antibody.
                                                                                                                                                                                                                               MSP-1; MSP-2;
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SSP-2;

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR66442
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Matches 23
Polypeptide inducing helper T cell, cytotoxic T cell and antibodies responses - to target antigen in hosts of different MNC haplotypes, esp. for therapeutic or prophylactications
                                                                                           WPI; 1995-006707/01.
                                                                                                                              Ahlers JD,
                                                                                                                                                              (USSH ) US DEPT
                                                                                                                                                                                                                                                       13-MAY-1994;
                                                                                                                                                                                                                                                                                            24-NOV-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T cell helper site; cytotoxic T cell response; neutralising antibody; P.falciparum CS antigen; circumsporozoite; malaria; vaccine.
                                                                                                                                                                                                                     14-MAY-1993;
                                                                                                                                                                                                                                                                                                                              WO9426785-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               03-AUG-1995
                                                                                                                                                                                                                                                                                                                                                                                                      Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR66442;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR66442 standard; peptide; 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), Iver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present sequence is the antigenic epitope P593, derived from circumsporozoite protein (CSP) of the sporozoite stage of plasmon falciparum. It is used in the construction of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vacous construction of the construction of recombinant protein construction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum, CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 2; Page 16; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100 nes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KPKDELDYENDIEKKICKMEKCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               falciparum circumsporozoite antigen
                                                                                                                        Berzofsky JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                      T HEALTH & HUMAN SERVICES.
DEPT HEALTH.
                                                                                                                                                                                                                9305-0060988
                                                                                                                                                                                                                                                 94WO-US05142.
                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
22..41
/label= repeat_reqi
                                                                                                                                                                                                                                                                                                                                                           /label= repeat_region
/note= "(NANP)5"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%;
                                                                                                                       Nara P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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Pred. No. 8.4e-12;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A
                                                                                                                   Pendleton
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        multistage malarial vaccine.
                                                                                                                 Ĝ
                                                                                                               Shirai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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PA
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AAR13175
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local :
WPI; 1991-179771/25.
                         Gross MS,
                                             (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST
                                                                                                  08-DEC-1989;
                                                                                                                          06-DEC-1990;
                                                                                                                                                  19-JUN-1991
                                                                                                                                                                          EP432965-A.
                                                                                                                                                                                                                                                                                                                                                                                        Key
Region
                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                        Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NS1_81-RLfdelta9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR13175 standard; Protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                           Influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                               hybrid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR13175
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
nybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The peptide AAR66442 was synthesised to make a peptide vaccine which is recognised by a broad range of MHC types that will elicit a T helper cell response, a CTL response and a high titre neutralising antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 4; Page 54; 120pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 KPKDELDYENDIEKKICKMEKCS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ch 100.0%; 1 Similarity 100.0%; 23; Conservative
                      Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                     falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first
                                                                                               89US-0447746
                                                                                                                       90EP-0313257
                                                                                                                                                                                                                                                                                        /note=
89..19
                                                                                                                                                                                                                                                                                                                                                    /note-
82..87
                                                                                                                                                                                              /label- AAs 297-412 of CS protein
/note- "Region II flanking region
inal AAs"
                                                                                                                                                                                                                                      194..309
                                                                                                                                                                                                                                                                                                                                                                                                                       (A/PR/8/34/).
                                                                                                                                                                                                                                                             /note≃ "Region
                                                                                                                                                                                                                                                                    /label - AAs 19-123 of CS
                                                                                                                                                                                                                                                                                                             'label- artifact
                                                                                                                                                                                                                                                                                                                                                    /label= N-terminal of NS1
/note= "Influenza virus nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                    label- synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entry)
                    Hollingdale MR;
                                                                                                                                                                                                                                   kegion l contg. flanking
signal sequence"
                                                                                                                                                                                                                                                                                               "see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66
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Pred. No. 2.7e-11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                         region
                                                                                                                                                                                                        minus 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                        less
                                                                                                                                                                                                      N-term-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          66;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
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Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.

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망
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR07945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ouery Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
New polypeptide used in malaria vaccine - comprises immunogenic determinants from 1st and 2nd flanking regions of plasmodium surface protein and intermediate repeat domain
                                                                        WPI; 1990-350299/47.
N-PSDB; AAQ06580.
                                                                                                                      Gross MS, Young JF;
                                                                                                                                                                                         03-MAY-1989;
                                                                                                                                                                                                                          01-MAY-1990;
                                                                                                                                                                                                                                                           22-NOV-1990.
                                                                                                                                                                                                                                                                                             EP398540-A.
                                                                                                                                                                                                                                                                                                                                             Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAS of the N-terminal of NS1 (NS1_81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking regionless the 18 AA signal region, which in turn is fused to DNA encoding Region II-contg. flanking region less the first nine N-terminal AS. This CS fusion is designated RLfdelta9. The Pro residue separating the Asp (at the C-terminal Site. The peptide can be used in a vaccine for protection against
                                                                                                                                                         (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                            Doma in
                                                                                                                                                                                                                                                                                                                                                                                                                           Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR07945 standard; protein; 319 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NS181RLFAuth plasmid product
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-FEB-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAR07945
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          See also AAR12306-R12311 and AAR13176-R13179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Example 1; Page 7; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ۵
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               l Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                      8908-0346863
                                                                                                                                                                                                                       90EP-0304720
                                                                                                                                                                                                                                                                                                                                                      label Fragment of circumsporozite protein
                                                                                                                                                                                                                                                                                                                                                                           /label= NS181 protein fragment
/note= "from plasmid pMG-1"
39..193.
                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%;
                                                                                                                                                                                                                                                                                                                    Fragment of circumsporozite protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 127; DB 12;
Pred. No. 1.5e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
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Example 2; Page 11-12; 24pp; English

Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.

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YXX PA PA XXX PA XXX PA XXX
                                                                                                                                                    PXPXPX
                                                                                                                                                                                                                     7777
                                                                                                                                                                                                                                                                777
                                                                                                                                                                                                                                                                                                                                                                                                         FEXOSXXX
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   δÃ
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                             Gross MS,
                                      WPI; 1991-179771/25.
                                                                                (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST
                                                                                                                            08-DEC-1989;
                                                                                                                                                  06-DEC-1990;
                                                                                                                                                                                         EP432965-A.
                                                                                                                                                                        19-JUN-1991
                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                        Region
                                                                                                                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                        Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Immunogenic determinant; circumsporozoite; CS; vaccine;
hybrid; influenza virus; non-structural protein 1; fusic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR13176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13176 standard; Protein; 319
                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NS1_81-RLfAuth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The product is useful in preparation of vaccines for treatment and prophylaxis of plasmodium sporozite infection. It may be easily produced in large pure quantities from a transformed E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  expression system.
                                                                                                                                                                                                                                                                                                                                                                                                                                         ntluenza virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      y Match 100.0%;
Local Similarity 100.0%;
hes 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            u
                                                          Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              319 AA;
                                                                                                                           89US-0447746
                                                                                                                                                 90EP-0313257
                                                                                                                                                                                                                                                                                                              /note=
89..19
                                                                                                                                                                                                                                                                                                                                                                                                                                      (A/PR/8/34):
                                                                                                                                                                                                              /label= AAs 288-412 of CS protein
/note= "Region II flanking region"
                                                                                                                                                                                                                                         note="see comments"
95..319
                                                                                                                                                                                                                                                                                'label= AAs 19-123 of CS protein
'note= "Region 1 contg. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                            /note-
                                                                                                                                                                                                                                                                                                                                                                              'note- "Influenza virus nonstructural protein l"
                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                           'label- artifact
                                                                                                                                                                                                                                                                                                                                      'label= artifact
                                                                                                                                                                                                                                                                                                                                                                                             'label- N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                            label- synthetic linker
                                                                                                                                                                                                                                                                                                                          "see comments"
                                                          Hollingdale
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 127; DB 11;
Pred. No. 1.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           319;
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В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural C protein 1 (NSI), [Beze et al., Nucleic Acids Research, 8: 5845] (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI (NSI_81) is linked via a synthetic sequence to DNA encoding Region C [C (NSI_81)] is linked via a synthetic sequence to DNA encoding Region C [C (NSI_81)] is linked via a synthetic sequence to DNA encoding Region C [C (NSI_81)] is linked via a synthetic sequence to DNA encoding Region C [C (NSI_81)] is linked via a synthetic sequence to DNA encoding Region C [C (NSI_81)] is linked via a synthetic sequence to DNA encoding Region II conts is fused to DNA encoding Region II-conts [I seed to Separating Region I and Region II-conts [I seed to BamHI site; the Gly separating Region I and Region II-conts [I seed to Separating Region I and Region II linker. The peptide can be used in a vaccine for protection against malaria.

The complete nucleotide and AA sequences are given in EP-304720, See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity
EP432965-A.
                                                                                                                                                   Region
                                                                                     Region
                                                                                                                                                                                                                   Region
                                                                                                                                                                                                                                                                                                       Region
                                                                                                                                                                                                                                                                                                                                                                     Region
                                                                                                                                                                                                                                                                                                                                                                                                            Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NS1_81-RLfAuth
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR13177 standard; Protein; 327 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Immunogenic determinant; circumsporozoite; CS; vaccine; hybrid; influenza virus; non-structural protein 1; fusi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAR13177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                          /label= AAs 19-123 of CS protein /note= "Region 1 contg flanking region less signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (A/PR/8/34/).
                                                                                   /note="see comments" 203..327
                                                                                                                                                            /label= immunodominant repeat region
/note= "two tetrapeptide repeat units"
                                                                                                                             /label= artifact
                                                                                                                                                                                                                   194..201
                                                                                                                                                                                                                                                                                                                    /note= "see comments"
                                                                                                                                                                                                                                                                                                                                          /label- artifact
                                                                                                                                                                                                                                                                                                                                                                                                                            /label= N-terminal of NS1
/note= "Influenza virus n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                  'label synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  18pp; English.
                                   - AAs 288-412 of CS protein 
"Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 127; DB 12;
Pred. No. 1.6e-10;
Nismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                     virus nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              malaria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319;
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RESULT
AAR13178
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
                                                                                              Key
Region
                Peptide
                                                       Region
                                                                                                                                                   Plasmodium falciparum
                                                                                                                                                                        Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                     NS1_81(NANP)4RLfAuth
                                                                                                                                                                                                                                               29-AUG-1991
                                                                                                                                                                                                                                                                          AAR13178;
                                                                                                                                                                                                                                                                                                  AAR13178 standard; Protein; 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                        [nfluenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM
(USSA ) US SEC OF THE ARMY
(BIOM-) BIOMEDICAL RES INS
                                                                                                                                                                                                                                                                                                                                                                  283 kpkdeldyendiekkickmekcs 305
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                            1 KPKDELDYENDIEKKICKMEKCS 23
                                                                                                                                                                                                                                                                                                                               7
                                                                                                                                                                                                                                                                                                                                                                                                                        L Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3; Page 10; 18pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          327 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                             (first entry)
                                                                                                                                     (A/PR/8/34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  90EP-0313257
                          note "four tetrapeptide"
                                                                    /note-
                                                                                                           Location/Qualifiers
'label= synthetic linker
                                         label-
                                                                               'label N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%;
                                                                "Influenza virus nonstructural protein
                                    immunodominant repeat region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 127; DB 12;
Pred. No. 1.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                             327;
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Best Local S
Matches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match .

Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRAIN-FCC1/HN;
Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
Molecular cloning and sequence analysis of major merozoite surface antigen(gp195)gene of plasmodium falciparum isolate FCC1/HN.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF218248; AAF27526.1; -.
                                                                                                                                                                                                                                                                                                                            Jiang G., Liu R.2., Daubenberger C.A., Pluschke G.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF062348; AAC72884.1; -: Interpro; IPR000561; EGF-11ke. Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1009
                                                              SEQUENCE FROM N.A.
                                                                                Eukaryota; Alveolata;
NCBI_TaxID=5833;
                                                                                                  Plasmodium falciparum
                                                                                                                      MAJOR MEROZOITE
                                                                                                                                                                                                                                                                                                                                                                            STRAIN-HN1;
                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
                                                                                                                                                                        1XHN60
                                                                                                                                                                                                                                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                      Merozoite
                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
MEROZOITE SURFACE PROTEIN 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9TZT5
                                                                                                                                                                                                                       995
                                                                                                                     1-OCT-2000 (TIEMBLIEL 15,
1-OCT-2000 (TIEMBLIEL 15,
1-JUN-2001 (TIEMBLIEL 17,
NJOR MEROZOITE SURFACE ANT)
                                                                                                                                                             )NHX1;
                                                                                                                                                                                                                                                                                                                                                                                      EQUENCE FROM N.A.
                                                                                                                                                                                                                                        -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13
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                                                                                                                                                                                                                    QYIKANSKFI-GITE
|::|:|| | |:||
QFVKSNSKVITGLTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QYIKANSKFI-GITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              QFVKSNSKVITGLTE 1023
                                                                                                                                                                                                                                                           Similarity 60. 9; Conservative
                                                                                                                                                                                                                                                                                                            1694 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1087 AA;
                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                    57.4%;
                                                                                                                                                                                                                     1009
                                                                                                                                                                                                                                        14
                                                                                                                                                                                                                                                                                                           192794 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57.48;
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                                                                                         Apicomplexa;
                                                                                                                                                                                                                                                                                                                                                                                                                Apicomplexa;
                                                                                                                      ANTIGEN.
                                                                                                                             Last sequence up
                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation updat
PRECURSOR.
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                                                                                         Haemosporida; Plasmodium
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Search completed: January Job time: 213 sec

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Pfam; PF00008; EGF; 1.
Merozoite.
SEQUENCE 1694 AA; 1
1005
                                                                                                Jiang G., Liu R.Z., Daubenberger C.A., Pluschke G.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases EMBL; AF062349; AAC72885.1; -. Interpro; IPR000561; EGF-11ke. Pfam; PF00008; EGF; 1.
                                                                                SEQUENCE
                                                                                                                                                                       Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID-5833;
                                                                                                                                               STRAIN-HN2
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4; Mismatches
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/cgn2_6/ptodata/2/paa/US06_COMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No. 1 2 3 4 4 5	Score 97 97 54 54 48	Query Match 100.0 100.0 55.7 55.7 52.6 49.5	Ouery Match Length DB 100.0 16 2: 100.0 350 2: 55.7 277 27 55.7 281 1: 49.5 262 1: 49.5 262 1:	1 00 01 01 44 44 17 17 1	US-09-763-397A-3 US-09-763-397A-2 US-60-324-109-22535 US-60-312-544-9219 US-09-134-001C-3628 US-09-138-452A-646 US-09-438-185-608	
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1033,	Sequence 350, App	350, Ap	Sequence 8915, Ap	11384	Sequence 9205, Ap	14,		5931,		4940,	3835,	1167,	2877,		200,	15941,	15941,	4093,	4086	10,		20,	e 6204,	44074,	938, 1	7311,	7604,	5480,	6979,	7440,	7059,	4906,	4183,	7241,	

ALIGNMENTS

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; TYPE: PRT
; ORCANISM: Plasmodium falciparum
US-09-763-397A-3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 3, Application US/09763397A
GENERAL INFORMATION:
APPLICANT: The Government of the United States of America, as represented by the APPLICANT: Secretary of the Department of Health and Human Services, Centers for APPLICANT: Control and Prevention
                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-08-19
NUMBER OF SEC ID NOS: 26
SOFTWARE: PatentIn version 3.1
SEC ID NO 3
                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/763,397A CURRENT FILING DATE: 2001-02-16 PRIOR APPLICATION NUMBER: US 60/097,703 PRIOR FILING DATE: 1998-08-21 PRIOR APPLICATION NUMBER: PCT / US99/18869 PRIOR FILING DATE: 1000-00-10 / US99/18869
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Lal, Altaf A.
APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against Plasmodium Fa
FILE REFERENCE: 6395-57049
  1 KPLDKFGNIYDYHYEH 16
                                          100.0%; ilarity 100.0%; Conservative 0
                                        Score 97; DB 21; I
; Pred. No. 1.7e-08;
...cmatches 0;
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                                             Indels
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....LICANT: Stein, Jingdong

FILE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT

FILE REFERENCE: 38-10(52726)B

CURRENT APPLICATION NUMBER: US/60/324,109

CURRENT FILING DATE: 2001-09-21

NUMBER OF SEQ ID NOS: 33196

SEQ ID NO 22535

LENGTH: 277

TYPE: PRT
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; Sequence 22535, Application US/60324109
; GENERAL INFORMATION:
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LENGTH: 350
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CURRENT FILING DATE: 2001-02-16
PRIOR APPLICATION NUMBER: US 60/097,703
PRIOR FILING DATE: 1998-08-21
PRIOR APPLICATION NUMBER: PCT / US99/18869
PRIOR FILING DATE: 1999-08-19
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Ping Shi, Ya
APPLICANT: Hasnain, Seyed E.
TITLE OF INVENTION: Recombinant Multivalent Malarial Vaccine Against plasmodium Falc
FILE REFERENCE: 6395-57049
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cao, Yongwei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
                                                                                                                                                                             FEATURE:
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50 RPVGNFKNSYDYHYQ 64
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                                                                      Conservative
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US-09-198-452A-646
; Sequence 646, Application US/09198452A
; GENERAL INFORMATION:
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GENERAL INFORMATION:
APPLICANT: Lynn Doucette-Stamm et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC-007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 3628
LENGTH: 313
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SEQ ID NO 9219
LENGTH: 281
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Best Local (
APPLICANT: Griffais, R.

APPLICANT: Griffais, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragme
TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, pr
TITLE OF INVENTION: and treatment of infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 9219,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/134,001C CURRENT FILING DATE: 1998-08-13 PRIOR APPLICATION NUMBER: US 60/064,964 PRIOR FILING DATE: 1997-11-08 PRIOR APPLICATION NUMBER: US 60/055,779 PRIOR FILING DATE: 1997-08-14 US/07/08-14 US/07/0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: CDNA SEQUENCES AND USES FOR PLANT IMPROVEMENT FILE REFERENCE: 38-10(52726)A CURRENT APPLICATION NUMBER: US/60/312,544

CURRENT FILING DATE: 2001-08-15
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APPLICANT: Edgerton, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Glycine max
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50 RPVGNFKNSYDYHYQ 64
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                                                                                                                                                                                                                                                                                                                                                                                                                                             QPVDKFGEIYDLNPE 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Stein, Joshua
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hinkle, Gregory J
Kovalic, David K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Application US/60312544
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53.3%;
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US-09-328-352-7148
; Sequence 7148, Application US/09328352
; Sequence 7148, Application US/09328352
; GENERAL INFORMATION:
; APPLICANT: Gary L. Breton et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
; TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: G7C99-0340.
; CURRENT APPLICATION NUMBER: US/09/328,352
; CURRENT FILING DATE: 1999-06-04
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; SEQ ID NO 646
; LENGTH: 262
; TYPE: PRT
; ORGANISM: Chlamydia pneumoniae
US-09-198-452A-646
; TYPE: PRT ; ORGANISM: Acinetobacter baumannii US-09-328-352-7148
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SEQ ID NO 608
LENGTH: 262
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Matches
                                                     NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7148
LENGTH: 78
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APPLICANT:
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CURRENT FILING DATE: 1999-11-11
PRIOR APPLICATION NUMBER: US 60/108,279
PRIOR FILING DATE: 1998-11-12
PRIOR APPLICATION NUMBER: US 60/128,606
PRIOR FILING DATE: 1999-04-08
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233 RPIDGFGNIRGIHY 246
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nes 8; Conserv
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Local Similarity 57.1%;
nes 8; Conservative
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Mitchell, Wayne
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Davis, Ronald
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Pred. No.
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                                                                                                                                                           US-09-328-352-7241
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 557
LENGTH: 102
TYPE: PRT
Sequence 7241, Application US/09328352
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 5702
LENGTH: 134
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GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING
TITLE OF INVENTION: BAUWANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
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Best Local Similarity
Matches 7; Conserv
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Matches 9; Conserv
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113 PLEKFAQLVDYH 124
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58.3%;
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Pred. No. 23;
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Pred. No. 12;
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RESULT 14
US-09-328-352-7059
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Best Local Similarity
""tohes 7; Conserv
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US-09-328-352-4906
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US-09-328-352-4183
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                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4906
LENGTH: 146
TYPE: PRT
                                                                                                                                                                                                                                                                                                                       Sequence 4906, Application US/09328352
GENERAL INFORMATION:
APPLICANT: Gary L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
FILE REFERENCE: GTC99-03PA
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Best Local Similarity 58.3%;
Matches 7; Conservative
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CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 4183
LENGTH: 146
TYPE: PRT
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GENERAL INFORMATION:
APPLICANT: GRAY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AMD AMINO ACID SEQUENCES RELATING TO ACINETOBACTER
TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
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Best Local :
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| 120 PLEKFAQLVDYH 131
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                                                                     PLEKFAQLVDYH 136
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Pred. No.
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Search completed: January 29,
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US-09-328-352-7440
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; ORGANISM: Acinetobacter baumannii
US-09-328-352-7059
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Best Local S
Matches 7
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GENERAL INFORMATION:
APPLICANT: GATY L. Breton et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ACINETOBACTE TITLE OF INVENTION: BAUMANNII FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: GTC99-03PA
CURRENT APPLICATION NUMBER: US/09/328,352
CUBRENT FILING DATE: 1990-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/09/328,352
CURRENT FILING DATE: 1999-06-04
NUMBER OF SEQ ID NOS: 8252
SEQ ID NO 7059
LENGTH: 191
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Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                                                                              LENGTH: 209
TYPE: PRT
                                                                                          188 PLEKFAQLVDYH 199
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Pred. No. 53;
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2: /cgn2_6/ptodata/2/paa/US06_NEW_COMB.pep:*

3: /cgn2_6/ptodata/2/paa/US07_NEW_COMB.pep:*

4: /cgn2_6/ptodata/2/paa/US08_NEW_COMB.pep:*

5: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

6: /cgn2_6/ptodata/2/paa/US09_NEW_COMB.pep:*

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US-09-708-427-65145
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US-09-708-427-11604

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ALIGNMENTS	US-09-708-427-24796	US-09-708-427-24797	US-09-708-427-80348	US-09-708-427-69128	US-09-708-427-20518	US-09-708-427-20520	US-09-708-427-80349	US-09-708-427-69129	US-09-985-153-70	US-09-985-153-135	US-09-985-153-91	US-09-708-427-3642	US-09-708-427-3643	US-09-708-427-3644	US-10-015-127-9820	US-09-708-427-1464	US-09-708-427-17301	US-09-708-427-1465	US-09-708-427-17302
	Sequence 24796, A	Sequence 24797, A	Sequence 80348, A	Sequence 69128, A	Sequence 20518, A	Sequence 20520, A	Sequence 80349, A	Sequence 69129, A	Sequence 70, Appl	Sequence 135, App	Sequence 91, Appl	Sequence 3642, Ap	Sequence 3643, Ap	Sequence 3644, Ap	Sequence 9820, Ap	Sequence 1464, Ap	Sequence 17301, A	Sequence 1465, Ap	Sequence 17302, A
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RESULT 4
US-09-815-242-13229
; Sequence 13229, Application US/09815242
; GENERAL INFORMATION:
; APPLICANT: Haselbeck, Robert
; APPLICANT: Ohlsen, Kari L.
; APPLICANT: Zyskind, Judith W.
; APPLICANT: Wall, Daniel
; APPLICANT: Wall, Daniel
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: TITLE OF INVENTION: Xenorhabdus sp. Genome S
: FILE REFERENCE: 38-21(51847)
: CURRENT APPLICATION NUMBER: US/09/897,516
: CURRENT FILING DATE: 2001-06-29
: PRIOR APPLICATION NUMBER: US 60/215, 161
: PRIOR FILING DATE: 2000-06-30
: NUMBER OF SEQ ID NOS: 8409
: SEQ ID NO 5215
: LENGTH: 138
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APPLICANT: Xu, H. Howard TITLE OF INVENTION: Identification TITLE OF INVENTION: Prokaryotes
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Hinkle, Gregory J.
Huesing, Joseph E.
Krasomil-Osterfeld, I
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Yamamoto, Robert T.
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Slater, Steven C
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Pred. No. 4.9;
0; Mismatches
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                                                   of Essential Genes
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PRIOR APPLICATION NUMBER: 60/257,931
PRIOR FILING DATE: 2000-12-22
PRIOR APPLICATION NUMBER: 60/269,308
PRIOR ETLING DATE: 2001-02-16
PRIOR ETLING DATE: 2001-02-16
NUMBER OF SEQ ID NOS: 14110
SOFTWARE: FRASESEQ FOR WINDOWS VERSION 4.
SEQ ID NO 13239
LENGTH: 459
RESULT 4
US-09-708-427-11605
; Sequence 11605, Application US/09708427
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JSEQUENCE 21300, Application US/09708427

GENERAL INFORMATION:

APPLICANT: N. ALEXANDROV et al.

TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES.

TITLE OF INVENTION: THEREBY

TITLE REFERENCE: 2750-1243P
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Best Local S
Matches
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 21300
LENGTH: 1404
                                                                                                                                                                                           Matches
                                                                                                                                                                                                           Query Match
Best Local
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PRIOR PPLICATION NUMBER: 60/242,578
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-10-23
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
PRIOR FILING DATE: 2000-11-27
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PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
                                                                                                                                                                                                                                                                                                                                         NAME/KEY: misc_feature
LOCATION: 1.1404
OTHER INFORMATION: Xaa is any amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                          TYPE: PRT
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                                                                                                                    102 KPSKKYKKLYDYFFE 116
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                                                                                                                                                       1 KPLDKFGNIYDYHYE 15
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Pred. No. 66;
3; Mismatches
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Pred. No.
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66;
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19;
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RESULT 6
US-09-708-427-11603
; Sequence 11603, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINE
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Best Local S
Matches 7
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CURREWY APPLICATION NUMBER: US/09/708,427
CURREWY FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PATENTIN VERSION 3.1
SEQ ID NO 11604
LENGTH: 1517
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Best Local Similarity 46.7
Matches 7; Conservative
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SEQ ID NO 11605
LENGTH: 1420
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LOCATION: 1..1517
OTHER INFORMATION: Xaa is
NAME/KEY: misc_feature
LOCATION: 1..1517
OTHER INFORMATION: Ceres S
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTITITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: N. ALEXANDROV et al
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ORGANISM: Arabidopsis thaliana
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ORGANISM: Arabidopsis thaliana
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                                                                                                                                                 159 KPSKKYKKLYDYFFE 173
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                                                                                                                                                                                 1 KPLDKFGNIYDYHYE 15
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       SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
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Pred. No.
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72;
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67;
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RESULT 8
US-09-708-427-82968
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US-09-620-111B-8023
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Sequence 82968, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THEREBY
FILE REFERENCE: 2750-1243P
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/620,111B
CURRENT FILING DATE: 2000-07-21
NUMBER OF SEQ ID NOS: 9298
SEQ ID NO 8023
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GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 45.4%;
Best Local Similarity 46.7%;
Matches 7; Conservative
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Matches 6; Conservative
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SEQ ID NO 11603
LENGTH: 1519
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CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
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LOCATION: 1..41
OTHER INFORMATION: Ceres
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LOCATION: 1..1519
OTHER INFORMATION: Xaa is any amino
NAME/KEY: misc_feature
LOCATION: 1..1519
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LOCATION: 1.41
OTHER INFORMATION: Xaa is any
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Pred. No.
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Pred. No.
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72;
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; LOCATION: 1..359
; OTHER INFORMATION: Xaa is a
; NAME/KEY: misc_feature
; LOCATION: 1..359
; OTHER INFORMATION: Ceres Se
US-09-708-427-65147
Sequence 65146, Application US/09708427

GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TILE OF INVENTION: THEREBY
FILE REFEBERCE: 2750-1243p
CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 65146
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; Sequence 65147, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID
; TITLE OF INVENTION: THEREBY
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Best Local Similarity
Thehes 7; Conserv
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CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 8534
SOFTWARE: Patentin version 3.1
SEQ ID NO 65147
LENGTH: 359
TYPE: PRT
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Best Local S
Matches 6
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SEQ ID NO 82968
LENGTH: 249
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LOCATION: 1..249
OTHER INFORMATION: Xaa is any amino acid
NAME/KBY: misc_feature
LOCATION: 1..249
COTHER INFORMATION: Ceres Seq. ID 1961854
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ORGANISM: Zea mays subsp. mays
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les 6; Conserv
                                                                                                                                                                                                                                                                                                      4 DKFGNIYDYHYE 15
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                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                      42.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Seq.
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Pred. No.
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                               ID 1928281
                                                                                                                                                                                                                                                                                                                                          Mismatches
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US-09-708-427-65145

; Sequence 65145, Application US/09708427
; GENERAL INFORMATION:
; APPLICANT: N. ALEXANDROV et al.
; TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
; TITLE OF INVENTION: THEREBY
; FILE REFERENCE: 2750-1243P
; CURRENT APPLICATION: NUMBER: US/09/708,427
; CURRENT FILING DATE: 2000-11-09
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NAME/KEY misc_feature

LOCATION: 1.369

OTHER INFORMATION: Xaa is any amino acid

NAME/KEY: misc_feature

LOCATION: 1.369

OTHER INFORMATION: Ceres Seq. ID 1928280

US-09-708-427-65146
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                                                     CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2795
                                                                                                                                                                                              Sequence 2795, Application US/09708427 GENERAL INFORMATION: APPLICANT: N. ALEXANDROV et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS: 85364
SOFTWARE: PatentIn version 3.1
SEQ ID NO 65145
LENGTH: 395
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                 TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
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                     LENGTH: 442
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Zea mays subsp.
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nes 7; Conservative
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58.3%;
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Pred. No. 48;
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US-09-708-427-2793
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Best Local Similarity
"hes 7; Conserve
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Best Local Similarity
Thehes 7; Conserve
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                                                                                                                                                                                                                   Sequence 2793, Application US/09708427
GENERAL INFORMATION:
APPLICANT: N. ALEXANDROV et al.
                                                           NUMBER OF SEQ ID NOS: 85364
SOPTWARE: PatentIn version
SEQ ID NO 2793
LENGTH: 521
TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQ ID NO 2794
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                                                                                                                       CURRENT APPLICATION NUMBER: US/09/708,427
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
                                                                                                                                                                        TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID TITLE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTID FILE OF INVENTION: THEREBY FILE REFERENCE: 2750-1243P CURRENT APPLICATION NUMBER: US/09/708,427 CURRENT FILING DATE: 2000-11-09 NUMBER OF SEQ ID NOS: 85364 SOFTWARE: Patentin version 3.1
                             ORGANISM: Arabidopsis thaliana FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 497
TYPE: PRT
ORGANISM: Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: N. ALEXANDROV et al
NAME/KEY: misc_feature LOCATION: 1..521
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OTHER INFORMATION: Xaa
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OTHER INFORMATION: Xaa
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                                                                                                                                                                                                                                                                                                                                    241 KPLDHPADYFDYH
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53.8%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 62;
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                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                           Length 497
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RESULT 15
US-09-708-427-68198
Sequence 68198, Application US/09708427
GENERAL INFORMATION:
GENERAL INFORMATION: SEQUENCE-DETERMINED DNA FRAGMENTS AND CORRESPONDING POLYPEPTIDES
TITLE OF INVENTION: THERBBY
FILE REFERENCE: 2750-1243P
CURRENT FILING DATE: 2000-11-09
NUMBER OF SEQ ID NOS: 85364
SOFTWARE: Patentin version 3.1
SEQ ID NO 68198
LENGTH: 212
TYPE: PRT
ORGANISM: Zea mays subsp. mays
FEATURE:
NAME/KEY: misc_feature
LCCATION: 1. 212
OTHER INFORMATION: Xaa is any amino acid
NAME/KEY: misc_feature
LCCATION: 1. 212
OTHER INFORMATION: Ceres Seq. ID 1934091
US-09-708-427-68198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; OTHER INFORMATION: Xaa is any amino acid NAME/KEY: misc_feature ; LOCATION: 1..521 ; OTHER INFORMATION: Ceres Seq. ID 1809714 US-09-708-427-2793
Search completed: January 29, 2002, 10:58:07 Job time: 2503 sec
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                                                                                                                                             Query Match
Best Local Similarity
Thes 7; Conserve
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                                                                                          Вb
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Best Local Similarity 53.8%;
Matches 7; Conservative
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265 KPLDHPADYFDYH 277
                                                                                        44 DKFGNIY 50
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                                                                                                             4 DKFGNIY 10
                                                                                                                                                               Conservative
                                                                                                                                                             41.2%; Score 40; DB 5;
100.0%; Pred. No. 34;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 5; Length 521;
Pred. No. 65;
2; Mismatches 4; Indels
                                                                                                                                                             0; Indels · 0;
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RESULT
AAR13179
ID AAR1
XX
AC AAR1
XX
DT 29-A
XX
NS1_
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                                                                                                                                                                                                            The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1 (NS1,81) is linked to a synthetic sequence encoding four repeat units from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region I conty. Flanking a synthetic sequence to DNA encoding Region I conty. Flanking region less the 18 AA signal region. This is linked to DNA encoding Region II-conty. Flanking region. The pro residue separating the As (at the C-terminal of the linker) from the Region I-conty. CS flanking region is an artifact of a filled in Bamili site; the GJy separating the Region I and II-conty. CS flanking regions is an artifact of a synthetic FOKI/ThIII I linker. The peptide can be used in a vaccine for protection against malaria.
                                                                                                                                              Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                    Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gross MS, Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-DEC-1989;
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(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST
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NS1_81(NVDP)4RLfAuth
                 29-AUG-1991 (first entry)
                                      AAR13179;
                                                         AAR13179 standard; Protein; 335 AA
                                                                                                                                                                                             Sequence
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                                                                                                                                            cch 100.0%; Score 127; DB 12; similarity 100.0%; Pred. No. 1.7e-10; 23; Conservative 0; Mismatches 0;
                                                                                                                                                                                              335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               104
/label= artifact
/note= "see comme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-0447746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90EP-0313257
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="see comments"
211.-33
/label= AAs 288-412 of CS protein
/note= "Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      comments"
                                                                                                           -
                                                                                                                                                                Length 335;
                                                                                                                                              Indels
                                                                                                                                              0;
                                                                                                                                              Gaps
                                                                                                                                               0,
                             Query Match
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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: $93 (1984)], and the influenza virus non-structural protein 1 (NSI), [Baez et al., Nucleic Acids Research, 8: $845 (1980)]. The DNA encoding the 1st #81 AAs of the N-terminal of NSI (NSI_81) is linked to a synthetic sequence encoding four repeat units (the variant form) from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region I contg. flanking region less the 18 AA signal region. This is contg. flanking region less the 18 AA signal region. This is residue separating the Asp (at the C-terminal of the linker) from the Region I-contg. CS flanking region is an aftifact of a filleding hashing regions is an artifact of a synthetic Fokl/TthIII inker. The peptide can be used in a vaccine for protection against malaria.
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Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 5; Page 11; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Polypeptide comprising immunogenic determinants from P falciparum - for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM. (USSA ) US SEC OF THE ARMY. (BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  08-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19-JUN-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EP432965-A
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hybrid; influenza virus; non-structural protein 1; fusion.
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gordon DM,
  335 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .90EP-0313257
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  89US-0447746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label- immunodominant repeat region
/note- "four variant tetrapeptide repeat units"
98..103
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /label= N-terminal of NS1
/note= "Influenza virus nonstructural protein 1"
82..97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= artifact
/note="see comments"
211.335
/label= AAs 288-412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        105..209
/label= AAs 19-123 of CS protein
/note= "Region 1 conty. flanking region less
signal sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (A/PR/8/34).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /label= AAs 288-412 of CS protein
/note= "Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hollingdale MR;
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100.0%;

Score 127;

рв

12;

Length 335;

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9

Best Local

Similarity

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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; T-celcumsporzoite protein (25P; sporzoite surface protein-1; SSP-2; circumsporzoite protein-1; MSP-1; merozoite surface protein-1; MSP-1; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; liver stage antigen-1; LSA-1; merozoite binding antigen-175; mapical membrane antigen-1, AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAY70278 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                   Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant vaccine CDC/NIIMALVAC-1
                                                                                                                                                                                                                                 Claim 3; Page 43-44; 52pp; English.
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DB; AAZ51336.
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Clostridium tetani
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /label= Melittin_signal_peptide
/note= "Derived from Honey bee"
23.350
                                                                                                                                                                                                                                                                                                                                                                                                                            HEALTH & HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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mismatches 0;
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Best Local S
Matches 23
                                                 sequence of the CS gene (AAN81108) is from lambda-mpfl. A recombinant DNA molecule is claimed, comprising functional DNA coding sequence fused, in phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) pre-S2-S protein coding sequence. The functional DNA coding sequence comprises the Pre-S2 coding sequence, Pre-S1 coding sequence of Pre-S1-pre-S2 coding sequence, the CS protein coding sequence of Plasmodium, or a HIV coding sequence such as an HIV envelope gene sequence, e.g. HIV C7 protein coding region, HIV peptide 121 coding region, or HIV Dreesman peptide coding region.
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                                                                                                                                                                                                                                                                                                                                         WPI; 1988-229751/33
N-PSDB; AAN81108.
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                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                            (SMIK ) SMITH
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23; Conser
                                                                                                                                                                                                                                                                                    ding hepatitis B virus antigens and hybrids contg. them expression in yeast to obtain vaccines and bivalent
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211..286
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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Pred. No. 1.8e-10;
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Loc
Matches
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Q9TZT5;
Q9TZT5;
Q1-MAY-2000 (TrEMBLrel. 13, CI
Q1-MAY-2000 (TrEMBLrel. 17, LE
Q1-JUN-2001 (TrEMBLrel. 17, LE
MEROZOITE SURFACE PROTEIN 1 PI
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01-OCT-2000 (TrEMBLrel. I

01-OCT-2000 (TrEMBLrel. I

01-JUN-2001 (TrEMBLrel. I

MAJOR MEROZOITE SURFACE A
Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
"Molecular cloning and sequence analysis of major merozoite surface antigen(gp195)gene of Plasmodium falciparum isolate FCC1/HN.";
submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF218248; AAF27526.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Jiang G., Liu R.Z., Daubenberger C.A., Pluschke G.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF062348; AAC72884.1; -. InterPro; IPR000561; EGF-11ke. PF00008; EGF; 1.
                                                                                                                              STRAIN-FCC1/HN;
                                                                                                                                                                                           Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID-5833;
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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NON_TER 1087 1087
SEQUENCE 1087 AA; 123911 MW
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EMBL; X61930; CAA43932.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 QYIKANSKFI-GITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QFVKSNSKVITGLTE 1009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QFVKSNSKVITGLTE 1023
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9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1694 AA;
                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               57.4%;
60.0%;
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                                                                                                                                                                                                                                                                                                              15, Created)
15, Last sequence update)
17, Last annotation updat
                                                                                                                                                                                                                                                                                             ANTIGEN
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PRECURSOR.
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4; Mismatches
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Pred. No. 53;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 42.5;
Pred. No. 84;
                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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                                                                                                                                                                                                                   Haemosporida;
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                                                                                                                                                                                                                      Plasmodium.
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Search completed: January Job time: 213 sec

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Query Match
Best Local Similarity
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Q9TZT4
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Best Local
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  1005
                                                                                                              Jiang G., Liu R.Z., Daubenberger C.A., Pluschke G.; Submitted (APR-1998) to the EMBL/GenBank/DDBJ databases. EMBL; AF062349; AAC72885.1; -. InterPro; IPR000561; EGF-11ke.
                                                                                     Merozoite.
SEQUENCE
                                                                                                                                                                                Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
                                                                                                         Pfam;
                                                                                                                                                      STRAIN-HN2;
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                  MSP1
                                                                                                                                                                                                                        01-MAY-2000 (TrEMBLrel. 13, 01-MAY-2000 (TrEMBLrel. 13, 01-JUN-2001 (TrEMBLrel. 17, MEROZOITE SURFACE PROTEIN 1
                                                                                                                                                                                                                                                                         Q9TZT4
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Pfam; PF00008; EGF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                                                         995 QFVKSNSKVITGLTE 1009
          1 QYIKANSKFI-GITE
                                                                                                                                                                                                                                                                                                                                    1 QYIKANSKFI-GITE 14
QFVKSNSKVITGLTE
                                                                                                      PF00008; EGF;
                                                                                                                                                                                                                                                                                                                                                               Similarity 9; Conserv
                                                                                     1704 AA;
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                                      Conservative
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                                                                                                                                                                                                                                                                         PRELIMINARY;
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60.0%;
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                                                                                                                                                                                           Apicomplexa; Haemosporida; Plasmodium.
                                                                                     WW;
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                                                                                                                                                                                                                        Last sequence update)
Last annotation updat
PRECURSOR.
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                                              Score 42.5;
Pred. No. 85;
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Pred. No. 84;
                                     Mismatches
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                                                                                    385526D0DA56FD1D
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Best Local
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                     InterPro; IPR003597; Ig_cl.
InterPro; IPR003006; Ig_MHC.
InterPro; IPR003053; MHC_II_beta.
Pfam; PF00047; ig; 1.
Pfam; PF00047; ig; 1.
Pfam; PF0009369; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
SMART; SM00407; IGCl; 1.
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Q31590;
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01-NOV-1996 (7
01-JUN-2001 (7
MHC CLASS II.
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01-NOV-1999
01-JUN-2001
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NON_TER
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                  Salmo salar (Atlantic salmon).

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; lactinopterygii; Neopterygii; Teleostei; Euteleostei; Protacanthopterygii; Salmoniformes; Salmonidae; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Salvelinus namaycush (lake trout).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Actinopterygii; Neopterygii; Teleostei; Euteleostei,
Protacanthopterygii; Salmoniformes; Salmonidae; Sal,
NCBI_TaxID-8040;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SANA.
                                                                                                                                                                                                                             MHC CLASS
       Glycoprotein;
                                                                                                                                                                                                                                                                                                                             TISSUE-LEUKOCYTES;
                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID-8030;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Glycoprotein; MHC
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                                                                                                                                                                                                                                                                                                                                                 EQUENCE FROM N.
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                                                                                                                                                                                         DOMAIN.
SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHAIN.
                                                                                                                                                       BETA-1 DOMAIN INTERPRO FAMILY.; x70166; CAA49725.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   w
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QYIKANS---KFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EYIRFNSTVGKFVGYTEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AF130026; AAD20889.1; --
Pro; IPR000353; MHC_II_beta.
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10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PD000328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         II BETA 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6 (TrEMBLrel. 01, 06 (TrEMBLrel. 01, 01) (TrEMBLrel. 17, 01)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              71 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (TrEMBLrel. 12, (TrEMBLrel. 12, (TrEMBLrel. 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
       MHC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11;
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MHC_II_beta; 1.
         MHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8002 MW;
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II; Transmembrane.
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Last sequ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding functions in an unusually compact cryptomonad nucleomorph.", Submitted (AUG-1998) to the EMBL/GenBank/DDI EMBL; AJ010592; CAB40403.1; -
Hypothetical protein.
SEQUENCE 546 AA; 66218 MW; 73030500577777
                                                                                                                                                                                                                                                                                                                  Salmo salar (Atlantic salmon).
Eukaryota; Metazoa; Chordata; Craniata; Vertebr:
Actinopterygii; Neopterygii; Teleostei; Euteleo:
Protacanthopterygii; Salmoniformes; Salmonidae;
NCBI_TaxID=8030;
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Q31578;
InterPro; IPR000353; MHC_II_beta.
Pfam; PF00969; MHC_II_beta; 1.
ProDom; PD000328; MHC_II_beta; 1.
Glycoprotein; MHC; MHC II; Transn.
NON_TER 1 1
NON_TER 67 67
                                                                                                                                             Grimholt U., Olsaker I., Vries Lindstrom C., Lie O.;
Submitted (OCT-1993) to the EMBL/GenBank/DDBJ databases.
-I- MISCELLANEOUS: FOUND N-TERMINAL TO IMMUNOGLOBULIN AND MAJOR
HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).
-I- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN, BETA CHI
BETA-1 DOMAIN INTERPRO FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Guillardia theta (Cryptomonas phi).
Eukaryota; Cryptophyta; Cryptomonadaceae;
CCBI_TaxID=55529;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1999 (TrEMBLrel. 12, La 01-NOV-1999 (TrEMBLrel. 12, La HYPOTHETICAL 66.2 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9XG37 PRELIMINARY;
Q9XG37;
01-NOV-1999 (TrEMBLrel.
                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Last seque 01-JUN-2001 (TrEMBLrel. 17, Last annot (DB03) MHC CLASS II BETA 1 (FRAGMENT).
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"Aberrant telomeres,
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Gapop 10.0 , Gapext 0.5
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sp_virus:*
sp_vertebrate:*
sp_unclassified:*
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34.954 Million cell updates/sec
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1 QYIKANSKFIGITEL 15 	Query Match Best Local Similarity 55.6%; Pred. No. 1 Matches 10; Conservative 3; Mismatch	SEQUENCE 60 AA; 6776 MW; 5D4F34	otein; MHC; M	ProDom; PD000328; MHC_II_beta; 1.	<pre>InterPro; IPR000353; MHC_II_beta. Pfam; PF00969; MHC_II_beta; 1.</pre>	EMBL; L24953; AAA49597.1;	-!- SIMILARITY: TO CLASS II HISTOCOMPATIBILITY ANTIGEN,	-!- MISCELLANEOUS: FOUND N'TERMINAL TO IMMUNOGLOBOLIN AND HISTOCOMPATIBILITY COMPLEX DOMAIN (BY SIMILARITY).		Grimholt U., Olsaker I., Vries Linds	[1] SEQUENCE FROM N.A.	NCBI_TaxID=8030;	Actinopteryg11; Neopteryg11; Teleostel; Protacanthopteryg11; Salmoniformes: Sal	Eukaryota; Metazoa; Chordata; Craniata;	Salmo salar (Atlantic salmon).	CLASS II BETA 1 (17,	(Tremstrel 01,	PRELIMINARI,	
	Score 44.5; DB 7; Length 60; Pred. No. 1.2; ; Mismatches 2; Indels 3; Gaps	5D4F3449060940E2 CRC64;	orane.				MPATIBILITY ANTIGEN, BETA CHAIN,	IO IMMONOGLOBOLIN AND MASON	€.	I., Vries Lindstrom C., Lie O.;			Salmonidae: Salmo.			7).	Last annotation update)	Created) Created)	, , , , , , , , , , , , , , , , , , , ,	

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                                                                                                      The present sequence is the antigenic epitope P593, derived from circumsporozotic protein (CSP) of the sporozotic stage of plasmodium circumsporozotic protein (CSP) of the sporozotic stage of plasmodium confunction. It is used in the construction of recombinant protein confunction of recombinant protein comprises, melitin signal peptide, (His)6 tag, The recombinant protein (CSP), sporozotic surface protein-2 (SSP-2), circumsporozotic protein (CSP), sporozotic surface protein-1 (SSP-2), liver stage antigen-1 (LSA-1), merozotic surface protein-1 (MSP-1), MSP-2, abtal membrane antigen-1 (AAM-1), erythrocyte binding antigen-175 (RBA-175), rhopty associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   T cell helper site; cytotoxic T cell response; neutralising antibody; P.falciparum CS antigen; circumsporozoite; malaria; vaccine.
         Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle \,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                              Claim 2; Page 16; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94WO-US05142.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0060988
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-AUG-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Berzofsky JA,
                                                                                                                                                                                                                                                                                                                                                                               23 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAY-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          14-MAY-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9426785-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ahlers JD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR66442;
                                                                                                                                                                                                                                                                                                                                                                               Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
AAR66442
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Gaps
                                         The peptide AAR66442 was synthesised to make a peptide vaccine which is recognised by a broad range of MHC types that will elicit a T helper cell response, a CTL response and a high titre neutralising antibody response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= AAs 297-412 of CS protein
/note= "Region II flanking region minus 9 N-term-
inal AAs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1..81
/label= Nrterminal of NS1
/label= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Immunogenic determinant; circumsporozoite; CS: vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                         ó
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "see comments"
89..193
/label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking region less signal sequence"
                                                                                                                                                                                                                                Length 66;
                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                        100.0%; Score 127; DB 16; ilarity 100.0%; Pred. No. 2.7e-11; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             82..87
/label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
Example 4; Page 54; 120pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR13175 standard; Protein; 309 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label- artifact
                                                                                                                                                                                                                                                                                                                                            44 kpkdeldyendiekkickmekcs 66
                                                                                                                                                                                                                                                                                                                  1 KPKDELDYENDIEKKICKMEKCS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Influenza virus (A/PR/8/34/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0447746.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM. (USSA ) US SEC OF THE ARMY. (BIOM-) BIOMEDICAL RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              194..309
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gross MS, Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1991-179771/25.
                                                                                                                                                                                                                           Query Match
Best Local Similarity
Matches 23; Conserv
                                                                                                                                                        66 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NS1_81-RLfdelta9,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-DEC-1989;
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                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13175;
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Region
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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using sw model OM protein - protein search,

January 29, 2002, 10:21:42; Search time 310.82 Seconds (without alignments) 5.481 Million cell updates/sec Run on:

US-09-763-397A-6

1 KPKDELDYENDIEKKICKMEKCS 23 Perfect score: Sequence: BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

522463 seqs, 74073290 residues Searched: Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

| SIDSB/gcgdata/geneseq/geneseqp/AAl981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AAl981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AAl981.DAT:*
| SIDSB/gcgdata/geneseq/geneseqp/AAl981.DAT:*
| SIDSB/gcgdata/geneseq-geneseqp/AAl981.DAT:*
| SIDSB/gcgdata/geneseq-geneseqp/AAl991.DAT:*
| SIDSB/gcgdata/geneseq-geneseqp/AAl991.DAT:*
| SIDSB/gcgdata/geneseq-geneseqp/AAl991.DAT:*
| SIDSB/gcgdata/geneseq-geneseqp/AAl991.DAT:*
| SIDSB/gcgdata/geneseq-geneseqp/AAl993.DAT:*
| SIDSB/gcgdata/geneseq-geneseqp/AAl993.DAT:* /SID88/gcgdata/geneseg/genesegp/AA1994. DAT:*/SID88/gcgdata/geneseg/genesegp/AA1995.DAT:*/SID88/gcgdata/geneseg/genesegp/AA1995.DAT:*/SID88/gcgdata/geneseg/genesegp/AA1996.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1997.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1998.DAT:*/SIDS8/gcgdata/geneseq/geneseqp/AA1999.DAT:* /SIDS8/gcgdata/geneseq/geneseqp/AA1980. A_Geneseq_1101:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

/SIDS8/gcgdata/geneseq/geneseqp/AA2001.DAT:*

SUMMARIES

	Description	Plasmodium falcipa	Plasmodium falcipa	NS1_81-RLfdelta9.	NS181RLFAuth plasm	NS1_81-RLfAuth. P	NS1_81-RLfAuth + (NS1_81 (NANP) 4 RL.fAu	NS1_81 (NVDP) 4RLfAu	Recombinant vaccin	Seguence encoded b	CS protein of mala
	QI	AAY70282	AAR66442	AAR13175	AAR07945	AAR13176	AAR13177	AAR13178	AAR13179	AAY70278	AAP83144	AAP60416
	DB	21	16	12	11	12	12	12	12	21	6	7
	Match Length DB ID	23	99	309	319	319	327	335	335	350	411	412
an i	Match	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0	100.0
	Score	127	127	127	127	127	127	127	127	127	127	127
1	NO.	П	7	ľΩ	4	S	9	7	80	6	10	11

RTS protein. Synt	q papooue encoded p	RTS* protein. Syn	oit	P.falciparum deriv	CS Region II+ mime	Plasmodium falcipa	Circumsporozoite a	Sequence corresp.	Plasmodium cynomol	CS Region II+ mime	Circumsporozoite a	Plasmodium berghei	Human IL-2/ P. yoe	H		f modi	Plasmodium falcipa	Malaria circumspor	P. falciparum CS p	Malaria circumspor	Circumsporozoite h	T-cell stimulatory		Pathogen derived T	T helper cell (Th)	eg	Τ.	_	Τ.	Plasmodium falcipa		۳. س	Plasmodium falcipa
AAR37796	AAP80835	AAR37797	AAR07290	AAR87213	AAR71651	AAY70283	AAR71655	AAP61002	AAP70709	AAR71654	AAR07291	AAP93560	AAB07288	AAY99033	AAJ04118	AAP91504	AAR82586	AAR78920	AAR75955	AAR70912	AAW05612	AAW35440	AAY23252	AAY80071	AAY54553	AAY58777	AAB99706	AAG62428	AAG84517	AAG88269	AAG89366	AAB84447	AAB98457
14	O	14	11	16	16	21	16	7	œ	16	11	10	21	21	22	10	16	16	16	16	17	18	20	21	21	21	22	22	22	22	22	22	
424	412	424	180	40	20	21	14	19	402	19	168	272	478	19	20	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21	21
		95.3	4	S	59.1	S	∞	48.8		46.1	9	46.1	4	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7	41.7
127	123	121	120	96	75	71	62	62	60,5	58.5	58.5	58.5	56.5	53	53	53	53	53	53	53	53	53	. 53	53	53	53	53	53	53	53	53	53	53
12	13	14	15	16	17	18	19	20	21	22	23	24	25	26	27	28	29	30	31	32	33	34	35.	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

AAY70282 standard; peptide; 23 AA. AAY70282;

RESULT

(first entry)

06-JUN-2000

Plasmodium falciparum CSP antigenic epitope, P593.

Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;

T-cell epitope, tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; merozoite surface protein-1; MSP-1; apital membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.

Plasmodium falciparum

WO200011179-A1.

02-MAR-2000.

99WO-US18869. 19-AUG-1999; 98US-0097703. 21-AUG-1998; (NAIM-) NAT INST IMMUNOLOGY. (USSH) US DEPT HEALTH & HUMAN SERVICES.

Shi YP, Hasnain SE; Lal AA,

WPI; 2000-237654/20.

19-JUN-1991.

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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., CScience 225: 593 (1984)], and the influenza virus non-structural protein [NSI], [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAS of the N-terminal of NSI (NSI 81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking regionless the 18 AA signal region, which in turn is fused to DNA encoding Region II-contg. flanking regionless the 18 AA signal region, which in turn is fused to DNA encoding Region II-contg. flanking region. C This CS fusion is designated RLfAuth. The Pro residue separating the ASP (at the C-terminal of the linker) from RLfAuth is an artifact of a filled in BamHi site, the Gly separating Region I and C FokI/TthIII I linker. The peptide can be used in a vaccine for protection against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              89.193
/label- AAs 19-123 of CS protein
/note- "Region 1 contg. flanking region less
194..201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label- inmunodominant repeat region
/note- "two tetrapeptide repeat units"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label- AAs 288-412 of CS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 127; DB 12;
100.0%; Pred. No. 1.6e-10;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                               See also AAR12306-R12311 and AAR13175-R13179.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label- N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      32..87
/label= synthetic linker
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/note-"see comments"
203..327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label artifact
/note "see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR13177 standard; Protein; 327 AA
                                                                              Example 2; Page 10; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        275 kpkdeldyendiekkickmekcs 297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KPKDELDYENDIEKKICKMEKCS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum.
Influenza virus (A/PR/8/34/).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-AUG-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NS1_81-RLfAuth + (NANP)2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note=
                                                                                                                                                                                                                                                                                                                                                                                              319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP432965-A.
                                                                                                                                                                                                                                                                                                                                                  filed May
                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Mon Feb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Peptide
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Gaps

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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., the P. falciparum circumsporozoite (CS) protein [Dame et al., science 225 : 593 (1984)], and the influenza virus non-structural protein 1 (NSI), [Baez et al., Nucleic Acids Research, 8 : 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI (NSI_81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking region less the 18 AA signal region. This is linked to a synthetic sequence encoding two repeat units from the immunodominant region, which in turn is fused to DNA encoding to Region II-contg. flanking region. The Pror residue separating the Region II-contg. CS flanking region is an artifact of a filled-in BamHI site; the Gly separating the repeat units and the Region II-contg. CS flanking region is an artifact of a synthetic Fokl/TthIII I linker. The region is an artifact of a synthetic Fokl/TthIII I linker. The peptide can be used in a vaccine for protection against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                        Polypeptide comprising immunogenic determinants from P falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "Influenza virus nonstructural protein 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 327;
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/label= immunodominant repeat region
/note= "four tetrapeptide repeat units"
                                                                                                                                                                                                                                           for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%; Score 127; DB 12; 100.0%; Pred. No. 1.6e-10;
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/label= N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        98..103
/label= synthetic linker
                                                                                                                                                            Gross MS, Gordon DM, Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR13178 standard; Protein; 335 AA
                                                                                                                                                                                                                                                                          Example 3; Page 10; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 KPKDELDYENDIEKKICKMEKCS 23
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Influenza virus (A/PR/8/34).
                                                                                           (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
                                90EP-0313257
                                                             89US-0447746
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Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NS1_81(NANP)4RLfAuth.
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                                                               08-DEC-1989;
                                06-DEC-1990;
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100.0%; Score 127; DB 12; Length 309; 100.0%; Pred. No. 1.5e-10; 1ve 0; Mismatches 0; Indels 0; 1 KPKDELDYENDIEKKICKMEKCS 23 Conservative Local Similarity 23; Seguence Query Match Best_Loca Matches

; 0

Gaps

0;

265 kpkdeldyendiekkickmekcs 287 Db ò

AAR07945 standard; protein; 319 AA AAR07945; AAR07945 RESULT

NS181RLFAuth plasmid product (first entry) Plasmodium falciparum. Malaria; vaccine. 22-FEB-1991

1..81 /label= NS181 protein fragment /note= "from plasmid pMG-1" Location/Qualifiers Domain Domain

89 193 // Alabel - Fragment of circumsporozite protein 204 .319 /label= Fragment of circumsporozite protein Domain

EP398540-A.

22-NOV-1990.

01-MAY-1990;

89US-0346863. 03-MAY-1989;

90EP-0304720.

(SMIK) SMITHKLINE BEECHAM

Gross MS, Young JF; WPI; 1990-350299/47.

N-PSDB; AAQ06580.

New polypeptide used in malaria vaccine - comprises immunogenic determinants from 1st and 2nd flanking regions of plasmodium surface protein and intermediate repeat domain

Example 2; Page 11-12; 24pp; English

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Gaps
         The product is useful in preparation of vaccines for treatment and prophylaxis of plasmodium sporozite infection. It may be easily produced in large pure quantities from a transformed E.coli
                                                                                                                                                                                                                                                                                                               Immunogenic determinant; circumsporozoite; CS; vaccine; malaria; hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                          /note= "Influenza virus nonstructural protein 1" 32..87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Polypeptide comprising immunogenic determinants.from P falciparu; for vaccine against malaria infection in humans.
                                                                                                                           ;
0
                                                                                                   Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Region 1 contg. flanking region less signal sequence"
                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= AAs 288-412 of CS protein
/note= "Region II flanking region"
                                                                                                  Score 127; DB 11;
Pred. No. 1.6e-10;
Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                                                                                             1.81
/label= N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /label= AAs 19-123 of CS
                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= artifact
/note= "see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= artifact
/note="see comments"
195..319
                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                         AAR13176 standard; Protein; 319 AA
                                                                                                                                                          275 kpkdeldyendiekkickmekcs 297
                                                                                                                                              1 KPKDELDYENDIEKKICKMEKCS 23
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                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 23; Conservative 0;
                                                                                                                                                                                                                                                                                                                                                             Influenza virus (A/PR/8/34).
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(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST.
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                                                                319 AA;
                                            expression system
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A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
A Wanshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                            WEDLINE-2108566; PubMcd=11217851;

K Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,

K Kawai J., Shinagawa A., Shibata K., Konno H., Adachi J., Fukuda S.,

A Arakawa T., Hara A., Fukunishi Y., Konno H., Kando S., Yamanaka I.,

A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,

Ka Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,

Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,

Ka Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,

Kachi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kuchi P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,

Kachimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,

A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,

Balake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Balake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,

Balake J., Boffelli D., Hofmann M., Hune D.A., Kamiya M., Lee N.H.,

A Gustincich S., Hill D., Hofmann M., Hune D.A., Kamiya M., Lee N.H.,

Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
STRAIN-C57BL/6J; TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa;
Mammalia; Eutheria;
NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000050; PID_domain. Pfam; PF00640; PID; 1. SMART; SM00462; PTB; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Functional annotation of a Nature 409:685-690(2001). EMBL; AK014093; BAB29151.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21085660; PubMed=11217851;
Kawai J., Shinagawa A., Shibata K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mus musculus (Mouse)
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PROSITE; PS01179; PID; 1.
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InterPro; IPR002086; Aldehyde_dehydr
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Rodentia;
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57.1%;
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Sciurognathi; Muridae.
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                 Je Bonalou
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.va M., Lee N.H.,
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                                                    Plasmodium : Eukaryota;
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Q9YTK4;
01-MAY-1999
01-MAY-1999
                                                                        Q25961 PRELIMINARY; PRT; Q25961; Q25961; O1-NOV-1996 (TrEMBLrel. 01, Last s 01-JUN-2001 (TrEMBLrel. 17, Last s MAJOR SURFACE ANTIGEN (FRAGMENT).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR002086; Aldehyde_dehydr.
InterPro; IPR000050; PID_domain.
Pfam; PF00640; PID; 1.
SMART; SM00462; PTB; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; UNKNOWN_1
PROSITE; PS01179; PID; 1.
                                                                                                                                                                                                                                                                                      Albrecht J.-C., Fleckenstein B.;
Primary Structure of the Herpesvirus Ateles (
Submitted (AUG-1998) to the EMBL/GenBank/DDBJ
EMBL; AF083424; AAC95587.1;
SEQUENCE 899 AA; 103389 MW; 19440A7944DE29
SEQUENCE FROM N.A STRAIN-RO-71; MEDLINE=92275047;
                                                                                                                                                                                                                                                                                                                                                                                                Ateline herpesvirus 3. Viruses; dsDNA viruses,
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ORF 63.
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EMBL; AK017798; BAB30939.1; -.
MGD; MGI:1917926; 5730529006Rik
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Hayashizaki Y.;
                                                                                                                                                                                                                                                                                                                                            STRAIN-73
                                                                                                                                                                                                                                                                                                                                                        SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                        Gammaherpesvirinae;
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8; Conserv
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9; Conser
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                                                     falciparum.
Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   309 AA;
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   PubMed=1592091
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                                                                                                                                                                                                                                                                                                                                                                                        Rhadinovirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ringwald M., Rodriquez I., Sakamoto N.,
Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
K., Wang K.H., Weitz C., Whittaker C., Wilming L.
Shida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
                                                                                                                                                                                                                                           58.1%;
64.3%;
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                                                       Apicomplexa;
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Last
                                                                                      Last sequence update)
Last annotation update)
                                                                                                           Created)
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Pred. No.
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annotation
                                                       Haemosporida; Plasmodium
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SEQUENCE

67

AA;

7449 MW;

42771AEDBABA6626 CRC64;

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Best Local s
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Best Local
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01-OCT-2000
01-OCT-2000
01-JUN-2001
                                                                           SEQUENCE FROM N.A.
MEDLINE=20088830; Pubw
Stanley E., Walsh L.,
    Stanley E.,
                                      "Identification of four loci isolated from thermophilus phage genomes responsible for resistance.";
                                                                                                                           Streptococcus thermophilus
Viruses; dsDNA viruses, no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9CF66;
Q9CF66;
01-JUN-2001
01-JUN-2001
01-JUN-2001
   SEQUENCE FROM N.A.
Stanley E., Walsh
                               FEMS Microbiol. Lett.
                                                                       van Sinderen
                                                                                                                                                    ORF13
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EMBL; AE006391; AAK05713.1; -.

InterPro; IPR000182; Acetyltransf_GCN5.

Pfam; PF00583; Acetyltransf; 1.

Transferase; Complete proteome.

SEQUENCE 180 AA; 21022 MW; 6DBD1485
                                                                                                                    NCBI_TaxID=112023;
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01-JUN-2001 (TrEMBLrel. 17, Last
01-JUN-2001 (TEMBLrel. 17, Last
SPERMIDINE ACETYLTRANSFERASE (EC
                                                                                                                                                                                                                                                                                                                                                                                                 Weissenbach J., Ehrlich S.D., Sorokin A.,
"The complete genome sequence of the lactic ac:
lactis.";
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Weissenbach J., Ehrlich
                                                                                                                                                                                                                                                                                                                                                                                                                                      STRAIN=IL1403;
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
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9; Conservative
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9; Conser
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                                                                                                                                                                                                       PRELIMINARY;
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L., van der Zwet
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RNA stage; Tailed
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Last sequence update)
Last annotation update)
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Pred. No. 6.7;
1; Mismatches
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Pred. No. 2;
4; Mismatches
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Sinderen
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RESULT
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Best Local S
Matches 8
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Q9CRV4;
O1-JUN-2001 (TrEMBLrel. 17, Cr
O1-JUN-2001 (TrEMBLrel. 17, La
O1-JUN-2001 (TrEMBLrel. 17, La
3110030A04RIK PROTEIN (FRAGMEN
3110030A04RIK.
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Best Local S
Matches 8
                                                             Mus musculus (Mouse)
Eukaryota; Metazoa; (
Mammalia; Eutheria; F
SEQUENCE FROM N.A.
                                        NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Appl. Environ. Microbiol. 65:1891-1899(1999).
EMBL; AF109874; AA037103.1; -
InterPro; IPR001091; N4_MTase.
InterPro; IPR002295; D21N6_mtfrase.
InterPro; IPR002295; D21N6_mtfrase.
Pfam; PF015555; N6_N4_Mtase; 1
PRINTS; PR00506; D21N6MTPRASE.
PRINTS; PR00506; S21N4MTPRASE.
PRINTS; PR00508; S21N4MTPRASE.
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Q9XJEB;
Q1-NOV-1999 (TrEMBLrel. 12, Created)
Q1-NOV-1999 (TrEMBLrel. 12, Last sequence)
Q1-JUN-2001 (TrEMBLrel. 17, Last annotatio)
PUTATIVE TYPE II DNA METHYLTRANSFERASE.
Lactococcus lactis bacteriophage Tuc2009.
Viruses; dsDNa viruses, no RNA stage; Tail
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McGrath S., Seegers J.F., Fitzgerald G.F., van
"Molecular characterization of a phage-encoded
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lactococcus lactis."
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InterPro; IPR001091; N4_MTase.
InterPro; IPR002941; N6_N4_Mtase.
Pfam; Pf01555; N6_N4_Mtase; 1.
PRINTS; PR00506; D21N6MTFRASE.
PRINTS; PR00508; S21N4MTFRASE.
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Rodentia;
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57.1%;
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57.1%;
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Pred. No. 9.5;
2; Mismatches
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Sciurognathi;
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9.5;
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thi; Muridae;
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                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match 100.0%;
Best Local Similarity 100.0%;
Matches 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                        The Plasmodium CS gene was used to isolate peptides capable of inducing an immune response to the parasite. Peptide antigens be synthesised in pure form and used to generate an immune response in vaccination against malaria. The featured repeat units are claimed and must be present in copies of 2-1000.
AAR37796;
                                         AAR37796 standard;
                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Disclosure; Fig 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New immunologically active pure synthetic peptide(s) protection against infection by malaria parasite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USDC )
(USGO )
(USSA )
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    McCutchan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-JAN-1986
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        24-JUN-1985;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sporozoite; vaccination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CS protein of malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-JUN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAP60416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAP60416 standard; Protein; 412
                                                                                                                                                      26-JUN-1984;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              367
                                                                                       12
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DB; AAN60362.
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US GOVERNMENT.
US SEC OF THE ARMY.
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                                                                                                                                                                                                                                                                                                                                                                             412
                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= Repeat unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 49pp; English.
                                         Protein; 424 AA.
                                                                                                                                                                                                                                              100.0%; Score 127; DB 7; 100.0%; Pred. No. 2.1e-10; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0,
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Pred. %0. 2.1e-10;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JĽ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Schneider
                                                                                                                                                                                                                                                                                               Length 412;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 411;
                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
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The 23; Conservative

100.0%;

0, Score Pred.

Mismatches 127; No. 2

Indels Length

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DB 14; .2e-10;

424; 0

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                                          the RTS expression cassette. This hybrid protein which is encoded by the RTS expression cassette. This hybrid consisits of a methionine residue derived from S. cerevisiae TDH3 gene sequence, three amino acids, Met-Ala-Pro, derived from a nucleotide sequence created by the cloning procedure used to construct the hybrid gene, a stretch of 189 amino acids representing amino acids 210 to 398 of the circumsporozoite protien (CSP) of plasmodium falciparum strain 768, an amino acid Arg created by the cloning procedure, four amino acids, representing the four carboxy terminal residues of hepatitis B virus (HBV), adw serotype, preS2 protein, and a stretch of 226 amino acids specifying the S protein of HBV, adw serotype. This protein, and RTS* (see also AAR37797), may be combined with an adjuvant and used in a vaccine for preventing plasmodium infections.
Sequence
                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 5; 59pp; English.
                                                                                                                                                                                                                                                                                                                                                                             Hybrid protein comprising Pl
HBsAg - useful as a vaccine
                                                                                                                                                                                                                                                                                                                                                            Plasmodium infections
                                                                                                                                                                                                                                                                                                                                                                                                                                    N-PSDB; AAQ42566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-182494/22.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              16-NOV-1991;
27-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloning; ci
strain 7G8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RTS; expression cassette; hybrid protein; S. cerevisiae; TDH3; cloning; circumsporozoite protien; CSP; Plasmodium falciparum; strain 7G8; hepatitis B virus; HBV; adw serotype; pres2 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        De Wilde M;
424
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92US-0842694
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note= "Represents amino acids 210-398 of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Carboxy terminal amino acids serotype) preS2 protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "S protein of HBV (adw serotype)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ۵.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Derived from S. cerevisiae TDH3 gene sequence"
                                                                                                                                                                                                                                                                                                                                                                           Plasmodium circ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               falciparum"
                                                                                                                                                                                                                                                                                                                                                                         circumsporozoite protein and ting patients susceptible to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           from HBV (adw
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밁

163 kpkdeldyendiekkickmekcs 185

RESULT 13 AAP80835

AAP80835;

18-SEP-1990

(first entry)

AAP80835 standard;

protein;

412

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Query Match
Best Local
                                                                                                  transcription termination region. A suitable coding sequence comprises the 1215bp Stul-Rsal fragment of WR201 conto. the P. falciparum CS protein coding sequence, minus its first 50bp. Also claimed is a transformed host cell, a method of culturing the cell to produce CS, the protein, and a vaccine. The vector comprises a 192 bp Sau3A fragment coding for 16 tetrapeptide repeats of the P. falciparum CS protein derived from Sau3A digestion of a 1215 bp Stul-Rsal fragment of WR201 containing the P. falciparum CS protein coding sequence minus approx. Its first 50 bp, or two, three, four or more tandem copies of
                                                                                                                                                                                                                                    Plasmid WR201 was obtained from the Walter Reed Army Institute of Research, and results from insertion of a 2.3 kb EcoRI fragment from lambda mpfl encoding the complete CS protein gene P. falciparum into vector pUC8. A recombinant DNA vector is claimed, which comprises a DNA sequence contg. the coding sequence of the CS P. falciparum operatively linked to an expression control sequence. Prefd. expression control sequences include the yeast glyceraldehyde-3p-dehydrogenase gene (TDH3) promoter and the yeast ornithine carbamoyl transferase gene (ARG3)
                                                                                       containing the P. approx. its first such 192 bp Sau3A
                                                                                                                                                                                                                                                                                                                                                                                                                    Expression of P. falciparum circumsporozoite protein by yeast using recombinant DNA vector having coding sequence linked to
                                                                                                                                                                                                                                                                                                                                                                        Example 1; Fig 2a; 44pp; English
                                                                                                                                                                                                                                                                                                                                                                                                     expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1988-235171/33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            De Wilde M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       30-JAN-1987;
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 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                      sequence
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95
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 Score
Pred.
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DNA

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RESULT
AAR37797
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This sequence represents the RTS* hybrid protein which is encoded by the RTS* expression cassette. This hybrid consisits of a methionine residue derived from S. cerevisiae TDH3 gene sequence, three amino acids, Met-Ala-Pro, derived from a nucleotide sequence created by the cloning procedure used to construct the hybrid gene, a stretch of 189 amino acids representing amino acids 210 to 398 of the circumsporozoite protien (CSP) of Plasmodium falciparum strain NF54, an amino acid Arg created by the cloning procedure, four amino acids, pro-Val-Thr-Asn, representing the four carboxy terminal residues of hepatitis B virus (HBV), adw serotype, pre52 protein, and a stretch of 256 amino acids specifying the S protein of HBV, adw serotype This protein, and RTS (see also AAR37796), may be combined with an adjuvant and used in a vaccine for preventing, plasmodium infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cloning; cir
strain 7G8;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RTS; expression
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                                                                                                                                                                                                                                                          N-PSDB;
                                                                                                                                                                                                                                                                                              Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                     11-NOV-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9310152-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                    Hybrid protein comprising Plasmodium circumsporozoite protein HBsAg - useful as a vaccine for treating patients susceptible
                                                                                                                                                                                                                                                                       WPI; 1993-182494/22
                                                                                                                                                                                                                                                                                                                                                16-NOV-1991;
27-FEB-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       368
                                                                                                                                                                                 Disclosure;
                                                                                                                                                                                                          Plasmodium
                                                                                                                                                                                                                                                                                                                      (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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                                                                                                                                                                                                                                                          AAQ42567
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ression cassette; hybrid protein; S. cerev
circumsporozoite protien; CSP; Plasmodium
G8; hepatitis B virus; HBV; adw serotype;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           standard; Protein;
                                                                                                                                                                                                                                                                                              De Wilde
                                                                                                                                                                                                          infections
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                                                                                                                                                                                 Fig 9;
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92US-0842694
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                                                                                                                                                                                 59pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                "S protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Represents amino P. falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Derived from S. cerevisiae TDH3 gene sequence"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Carboxy terminal amino serotype) preS2 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Cloning artefact"
                                                                                                                                                                                 English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ИВV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 protein"
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Plasmodium falciparum;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                (adw serotype)"
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25-JAN-1988; 11-SEP-1988

88WO-BE00002

Region Region

WO8805817-A

кеу

location/Qualifiers

Region

148.

/note="repeat region, /note="repeat region, 148..207

/note="repeat region,

repeat unit-NANP" repeat unit-NANP" repeat unit-NANPNVDP' Plasmodium

falciparum

yeast yeast

Circumsporozoite gene; Plasmodium falciparum;

glyceraldehyde-3P-dehydrogenase
ornithine carbamoyl transferase

gene

(TDH3) promoter; (ARG3); repeat i

lambda mPfl; vaccine

carbamoy1

Sequence encoded by the circumsporozoite (CS) gene of Plasmodium falciparum in lambda mPfl.

Job time: 419 sec

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                                                                                                                                                                                                                                             RESULT 15
AAR07290
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                                                                                                          Query Match 94.5
Best Local Similarity 95.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match . 95.3
Best Local Similarity 95.7
Matches 22; Conservative
                                                                                                                                                                                                                                                                                                                               The protein was produced by expression of a synthetic gene. The analogue comprises AAs 68-123 of the native P. falciparum CS protein, followed by four repeat sequences (three "B"s, i.e. NANP) and one "A", i.e. NVDP), followed by AAs 289-392 of the native protein. Reduction of the immunological dominance of the repeats relative to the epitopes in the regions flanking the repeats
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 10; Fig 10; 22pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant plasmodium circumsporozoite analogues · lacking one or more repeat epitope(s) for use as a malaria sub-unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Circumsporozoite analogue Falciparum 4.
                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                           enhances sporozoite neutralising activity. See also AAR07287-91.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1990-314486/42.
N-PSDB; AAQ06153.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-APR-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EP392820-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CS protein; plasmodium; malaria; vaccine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28-JAN-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAR07290 standard; protein; 180 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Barr PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (CHIR-) CHIRON CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                17-OCT-1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAR07290;
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bathurst IC,
                                                                                                                                                                                                                                          180 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-0336288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90EP-0303907.
                                                                                                    94.5%; Score 120; DB 11;
95.7%; Pred. No. 8.6e-10;
tive 0; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95.3%;
95.7%;
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Pred. No. 1.6e-09;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HL;
                                                                                                                                                        DB 11;
                                                                                                                                                      Length 180;
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Search completed: January 29, 2002, 10:21:43

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Minimum DB seq
Maximum DB seq
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Scoring table: .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ş
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     protein -
             Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              d. No. is the number of results predicted by chance to have a re greater than or equal to the score of the result being printed, is derived by analysis of the total score distribution
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Issued_Patents_AA:*
1: /cgn2_6/ptodata/2
2: /cgn2_6/ptodata/2
3: /cgn2_6/ptodata/2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                length: 0
length: 2000000000
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                                                                                                                                                                    59.1
44.9
44.5
41.7
41.7
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95.3
66.9
64.6
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Gapop 10.0 ,
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127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                KPKDELDYENDIEKKICKMEKCS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /cgn2_6/ptodata/2/laa/5A_COMB.pep:*
/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/6A_COMB.pep:*
/cgn2_6/ptodata/2/laa/6B_COMB.pep:*
/cgn2_6/ptodata/2/laa/B_COMB.pep:*
/cgn2_6/ptodata/2/laa/BCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/backfiles1.pep:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           by analysis of the total score distribution
                                                  Gapext 0.5
   US-08-455-625-35
US-08-455-685-35
US-08-060-988A-35
PCT-US94-05142-35
US-08-313-288B-18
US-08-313-288B-18
US-08-32-299B-3
US-08-318-856A-75
US-08-318-856A-75
US-08-318-856A-76
US-08-318-856A-76
US-08-318-856A-76
US-08-466-592-48
US-08-466-592-48
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PCT-US95-03121-27
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US-08-486-351A-27
US-08-486-351A-27
US-08-486-351A-27
US-08-486-351A-27
US-08-318-856A-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23
                           Sequence 75, Appl
Sequence 76, Appl
Sequence 2, Appli
Sequence 6, Appli
Sequence 48, Appl
Sequence 48, Appl
Sequence 27, Appl
Sequence 28, Appl
Sequence 28, Appl
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Sequence 35, Appl
Sequence 35, Appl
Sequence 18, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 3, Appli
Sequence 3, Appli
Sequence 3, Appli
   Sequence
Sequence
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27, Appl
27, Appl
5, 5171843
20, Appl
28, Appl
25, Appl
21, Appl
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43	43.5	43.5	43.5	44	44	44	44	44	44	45	45	45	46	46.5	46.5	46.5	46.5
33.9	34.3	34.3	34.3	34.6	34.6	34.6	34.6	34.6	34.6	35.4	35.4	35.4	36.2	36.6	36.6	36.6	36.6
16	1264	1264	1264	3969	1400	1400	1400	714	607	9	8	œ	863	503	503	492	492
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US-08-817-933A-7	US-08-487-203A-6	US-08-005-002C-6	US-07-789-915A-6	US-08-061-376-5	PCT-US93-05857-7	US-08-465-713-7	US-08-080-255-7	US-08-472-534-3	US-08-472-534-5	US-08-318-856A-27	PCT-US95-02121-17	US-08-318-856A-3	US-09-238-303-11	US-08-990-571-52	US-08-845-258-52	US-08-723-142A-21	US-08-990-571-21
Sequence 7, Appli	Sequence 6. Appli	Sequence 6. Appli	σ.	.	7	Sequence 7. Appli	7	ω.	UI .		17	ω <u>!</u>	1	Sequence 52. Appl	52	Sequence 21. April	Sequence 21. Appl

ALIGNMENTS

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US-08-455-625-35
                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: SVENSSON, LEONARD R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 1173
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-205-8000
TELEPAX: 703-205-8050
INFORMATION FOR SEQ ID NO: 35:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Berzofsky, Jay A.
APPLICANT: Ahlers, Jeffrey D.
APPLICANT: Pendleton, C. D.
APPLICANT: Nara, Peter
APPLICANT: Nara, Peter
TITLE OF INVENTION: COMPOSITE
TITLE OF INVENTION: COMPOSITE
TITLE OF INVENTION: LYMPHOCYTE
TITLE OF INVENTION: LYMPHOCYTE
                                     MOLECULE TYPE: peptide FRAGMENT TYPE: internal FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIJIM TYPE: Floppy disk
COMPUTER: IBM Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 14-MAY-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
                                                                                            TYPE: ami
NAME/KEY: Peptide LOCATION: 1..66
                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: P.O. Box 7.
CITY: Falls Church
STATE: Virginia
                                                                                                                                    LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Virginia
COUNTRY: USA
ZIP: 22040-0747
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             35, Art 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION:
                                                                                               amino acid
GY: linear
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                                                                                                                                    66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Berzofsky, Jay A.
Ahlers, Jeffrey D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Birch, Stewart, Kolasch & Birch
O. Box 747
                                                                                                                                                                                                                                                                                                                                      14-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LYMPHOCYTES AGAINST HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT ELICITING NEUTRALIZING ANTIBODIES AND CYTOTOXIC
                                                                                                                                                                                                                                                                                                                                                    B86'090'80 sn
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; MOLECULE TYPE: US-08-455-685-35
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OTHER INFORMATION:
US-08-455-625-35
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US-08-455-685-35
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     Matches
                    Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 35, Application US/08455685
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local
                                                                                                                                                                                                                                                                                                              FILING DATE: 14-MAY-1993
APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: 07/148,692
APPLICATION NUMBER: 07/148,692
FILING DATE: 26-JAN-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                                                                     INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                NAME: Beattie, Ingrid A.
REGISTION NUMBER: P-42,3
REFERENCE/DOCKET NUMBER: 08
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617,542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Nara, Peter
APPLICANT: Shiral, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES THAT ELICIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES: 40
                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 66 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: Windows95
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Berzofsky, Jay A. APPLICANT: Ahlers, Jeffrey D. APPLICANT: Pendleton, C. David
                                                                                                                              LENGTH: 66 amino
TYPE: amino acid
                                                                                                                                                                                                      TELEPHONE: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/0 FILING DATE: 31-MAY-1995
                                                                                                                     TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 KPKDELDYENDIEKKICKMEKCS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              y Match 100.0%;
Local Similarity 100.0%;
hes 23; Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         02110-2804
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225 Franklin Street
     Conservative
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                                                                                                    peptide
                   100.0%;
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               Score 127; DB 4; Pred. No. 8.9e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 127; DB 2;
Pred. No. 8.9e-12;
   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                Length 66;
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 Indels
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0;
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Gaps
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0,
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PCT-US94-05142-35
; Sequence 35, Application PC/TUS9405142
; GENERAL INFORMATION:
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                                                              RESULT
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                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: 07/847,311
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/751,998
FILING DATE: 29-AUG-1991
APPLICATION NUMBER: 07/148,692
FILING DATE: 26-JAN-1988
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
APPLICANT
                                                                                                                                                                                                                                                                        TOPOLOGY: 1,i
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TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Nara, Peter
APPLICANT: Shirai, Mutsunori
TITLE OF INVENTION: MULTIDETERMINANT PEPTIDES
TITLE OF INVENTION: THAT ELICIT
TITLE OF INVENTION: HELPER T-LYMPHOCYTE, CYTOTOXIC T LYMPHOCYTE AND
TITLE OF INVENTION: NEUTRALIZING ANTIBODY RESPONSES AGAINST HIV-1
NUMBER OF SEQUENCES: 48
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
                                                                                                            44 KPKDELDYENDIEKKICKMEKCS 66
                                                                                                                                                                                          Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 14-MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM CONTROL OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Beattie, Ingr
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                           1 KPKDELDYENDIEKKICKMEKCS 23
                                                                                                                                                                                                                                                                                                                       LENGTH:
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                                                                                                                                                                                                                                                                                                        amino acid
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                                                                                                                                                                            Conservative
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Pendleton, C. David
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                                                                                                                                                                       Score 127; DB 4;
Pred. No. 8.9e-12;
Mismatches 0;
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                                                                                                                                                                                                         Length 66;
                                                                                                                                                                         Indels
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Patent No. 5750502
; GENERAL INFORMATION:
; APPLICANT: Jessell, T
TITLE OF INVENTION: N
TITLE OF INVENTION: N
                                                                                                                                                                                                                                                                                                          US-08-313-288B-18
                                                                                                                                                                                                                                                                                            Sequence
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Best Local Similarity
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INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION: ELLI-
TITLE OF INVENTION: LYM
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                        NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
NAME: Svensson, Leonard R.
REGISTRATION NUMBER: 30330
REFERENCE/DOCKET NUMBER: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 14-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY:
                                                                                         CITY: New York
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LOCATION: 1..66
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: PCT/
FILING DATE: 13-MAY-1994
CLASSIFICATION:
                                                         COUNTRY: UZIP: 10036
                                                                                                                                                                                                                                                                                                                                                                                 44 KPKDELDYENDIEKKICKMEKCS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                    1 KPKDELDYENDIEKKICKMEKCS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH:
                                                                                                                                                                                                                                                                             18, Application US/08313288B
o. 5750502
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Falls Church
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ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Peptide
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CLONING, EXPRESSION AND USES OF A
NOVEL SECRETED PROTEIN, F-SPONDIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPOSITE SYNTHETIC PEPTIDE CONSTRUCT ELICITING NEUTRALIZING ANTIBODIES AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Stewart, Kolasch & Birch
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LYMPHOCYTES AGAINST HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /label= peptide
/note= "peptide from P. falciparum CS antigen"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US 08/060,988
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Pred. No. 8.9e-12;
0; Mismatches 0;
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Best Local Similarity
Matches 23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1,
                                                                 APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 845015-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                          PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline
STREET: 709 Swedeland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: from Plasmodium and HBsAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 40028-A-PCT-US TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        368 KPKDELDYENDIEKKICKMEKCS 390
                                                                                                                                                                                                                            FILING DATE: 04-DEC-1996 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 709 Swedeland CITY: King of Prussia STATE: PA
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SOFTWARE: Patenti
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                                                                                                                                                                                                                                                             APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 19406
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX:
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                                                    610-270-5090
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                                                                                                       В45015-1С2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
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; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-08-760-797A-1
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                                                                                                                                    TOPOLOGY:
US-08-932-929B-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 1, Application US/08932929B
Patent No. 6169171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Matches
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                                                              Matches
                                                                                        Query Match
                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Hybrid Protein Between CS
                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/760,797
APPLICATION NUMBER: 08/442,612
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                162 KPKDELDYENDIEKKICKMEKCS 184
                                                                                                                                                                                                                                                                                 NAME: Baumeister, Kirk
REGISTRATION NUMBER: 33,833
REGISTRATION NUMBER: B45015-1FWC2
REFERENCE/DOCKET NUMBER: B45015-1FWC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity 100.
Les 23; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 KPKDELDYENDIEKKICKMEKCS 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: King of Prussia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/932,929B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
FILING DATE:
                                                                        Local
                                                                                                                                                                                                                                                                                TELEPHONE:
                                                                                                                                                                                                                                                                  TELEFAX:
                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                     TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19406
                                                              L Similarity
23; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3: SmithKline Beecham Corporation
709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cohen, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          De Wilde, Michel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                  610-270-5090
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                                                              Conservative
                                                                                                                                                          linear
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                                                                                                                                                                        single
                                                              100.0%; Score 127; DB 4; 100.0%; Pred. No. 6.5e-11; tive 0; Mismatches 0;
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                                                                                                  Length 424;
                                                                    Indels
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RESULT

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US-08-760-797A-3
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                                                                                                                                                                                                                                                                                                RESULT
                                                                                                                                                                                                                                                                                 US-08-932-929B-3
                                                                                                                                                                                                                                              Sequence 3, Application US/08932929B Patent No. 6169171
                                                                                                                                                                                                                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local
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                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
COMPUTER: IBM Compat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBSAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister; Kirk
REGISTRATION NUMBER: 33,833
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: (FILING DATE: 04-DEC-CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: B4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                               APPLICANT: De Wilde, Michel APPLICANT: Cohen, Joseph
                                                                                                                                                                                                                                                                                                                                            1 KPKDELDYENDIEKKICKMEKCS 23
|||||||| |||||||||||||
159 KPKDELDYANDIEKKICKMEKCS 181
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COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                TITLE OF INVENTION: Hybrid Protein Between CS
                                                                                                                                CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH:
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                                                                                                                                                   NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: amino acid STRANDEDNESS: sin
                                  COUNTRY: U:
ZIP: 19406
                                                                STATE:
                                                                                 CITY: King of Prussia
                                                                                                 STREET:
                                                                                                 ADDRESSEE: SmithKline Beecham Corporation STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19406
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                                                                                                                                                                                                                                                                                                                                                                                                                              Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           424 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
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95.7%;
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Pred. No.
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Gaps

0;

SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:

OPERATING

IBM Compatible SYSTEM: DOS

APPLICATION NUMBER: US/08/932,929B

FILING DATE:

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RESULT 11
US-08-318-856A-75
; Sequence 75, Application US/08318856A
; Patent No. 5972351
. GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 10
5178861-7
;PATENT NO. 5178861
; APPLICANT: VERGARA, ULISES;RUIZ, ANDRES;FERREIRA, ARTURO;
;NUSSENZWEIG, RUTH S.: NUSSENZWEIG, VICTOR N.
; TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES
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NUMBER OF SEQUENCES: 18
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                            SEQ ID NO:7:
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Best Local Similarity
Matches 22; Conserv
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ATTORNEY/AGENT INFORMATION:
NAME: Baumeister; Kirk
REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: 8450
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/08/370,241 FILING DATE: 22-JUN-1989 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/7
FILING DATE: 04-DEC-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                159
                                                                                                                                       16
                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
                                                                                                                                                                                                                 Local Similarity
                                                                                                                                    1 KPKDELDYENDIEKKIC 17
|||||| |||||||||
16 KPKDELIYENDIEKKIC 32
                                                                                                                                                                                                                                                                                                                             FILING DATE: 12-SEP-1984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: 08/4
                                                                                                                                                                                                                                                                                              LENGTH: 32
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                                                                                                                                                                                                16;
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94.1%;
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95.7%;
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Pred. No. 4.8e-10;
                                                                                                                                                                                             Score 85; DB 6;
Pred. No. 4.8e-06;
0; Mismatches 1
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                                                                                                                                                                                                                           Length 32;
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                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1+
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/318,856,
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO: 75:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Adrian V.
TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                           APPLICANT: Adrian v.S. Hill, et al.
TITLE OF INVENTION: PLASMODIUM FALC
TITLE OF INVENTION: RESTRICTED CTL
TITLE OF INVENTION: ANTIGENS (AS AM
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REGISTRATION NUMBER: 40,949
REFERENCE/DOCKET NUMBER: 26
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: AUGUST 20, 1992
PRIOR APPLICATION DATA:
APPLICATION NILPARY
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P.
STREET: 2033 K Street, N.W., Suite 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: WO PCT/GB93/00711
FILING DATE: April 5, 1993
ATTORNEY/AGENT INFORMATION:
NAME: Lee Cheng
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: GB 92 08 068.8 FILING DATE: APRIL 3, 1992 PRIOR APPLICATION DATA: APPLICATION NUMBER: GB 92 17 704.7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44
                             COUNTRY: U.S.A.
                                               STATE:
                                                                                STREET:
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CITY: Washington
                                                                                              ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                     ENDIEKKICKMEKCS 15
                   20006
                                                           Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    amino acid residues
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                                               D.C.
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                                                                             E: Wenderoth, Lind & Ponack, 2033 K Street, N.W., Suite 80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Adrian V.S. Hill, et al.
VENTION: PLASMODIUM FALCIPARUM MHC CLASS I-
VENTION: RESTRICTED CTL EPITOPES DERIVED FROM PRE-ERYTHROCYTIC STAGE
VENTION: ANTIGENS (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                            PLASMODIUM FALCIPARUM MHC CLASS
RESTRICTED CTL EPITOPES DERIVED
ANTIGENS (AS AMENDED)
                                                                                                                                                                                                                                                                                                                                                                                                                     64.6%;
100.0%;
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
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FROM PRE-ERYTHROCYTIC
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RESULT
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5178861-18
;Patent No. 5178861
                                                                                                                                                                                                                                                                                                                                                                        5178861-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: VERGARA, ULISES; RUIZ, ANDRES; FERREIRA, ARTURO; RUSSENZWEIG, VICTOR N.
TITLE OF INVENTION: CROSS-REACTIVE AND PROTECTIVE EPITOPES; OF CIRCUMPOROZOJIE PROTEINS
UNUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                              :SEQ ID NO:18:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk, 3.5 inch, 1.44 mb
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC CDS/MS-DOS
SOFTWARE: WOTGPERICET 5.1+
CUBRENT APPLICATION DATA:
APPLICATION UMBER: US/08/318,856A
FILING DATE: October 3, 1994
PRIOR APPLICATION DATA:
APPLICATION UMBER: GB 92 08 068.8
FILING DATE: APFIL 3, 1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: APFIL 3, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: AUGUST 20, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: AUGUST 20, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: AUGUST 20, 1992
PRIOR APPLICATION NUMBER: GB 92 17 704.7
FILING DATE: APGING DATE: 
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Best Local Similarity
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acid residues
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/
FILING DATE: 22-JUN-1989
PRIOR APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: 263-PPIR1577US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 115,634
FILING DATE: 26-OCT-1987
APPLICATION NUMBER: 649,903
FILING DATE: 12-SEP-1984
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1 ELDYANDIEKKICKM 15
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                                                                                    KPKDELIYENDI 18
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91.78;
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Pred. No.
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Pred. No.
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US-08-186-266-6; Sequence 6, Applic; Patent No. 5662907
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Spevack, A. David
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: N.C.
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202):295-6759
                                                                                                                                                TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOSTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Hedstrom, Richard C.
APPLICANT: Sedegah, wartha
TITLE OF INVENTION: EQLYNUCLECTIDE VACCINE PROTECTIVE
TITLE OF INVENTION: AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR
TITLE OF INVENTION: DELIVERING POLYNUCLECTIDE VACCINES
                                                                                                                                                                                                                          APPLICANT: KUBO, Ralph T.
APPLICANT: GREY, Howard M.
APPLICANT: SETTE, Alessandro
APPLICANT: CELIS, Esteban
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
ZIP: 94105-1493
COMPUTER READABLE FORM:
                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend Khourie and Crew
STREET: Steuart Street Tower, One Market Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                           435 KQPENLTLE-DIDTEICKMDKCS 456
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                                                STREET: Steuart Stre
CITY: San Francisco
STATE: California
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ZIP: 20889-5606
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CITY: Bethesda
STATE: Maryland
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                                    COUNTRY:
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Bldg. 1, T-12 8901 Wisconsin Ave.
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Hedstrom, Richard C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                          T LYMPHOCYTES
                                                                                                                                                                         SYNTHETIC PEPTIDE
                                                                                                                                                                                          INDUCTION OF ANTI-TUMOR CYTOTOXIC T LYMPHOCYTES IN HUMANS USING
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Pred. No. 1.1;
4; Mismatches
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MEDIUM TYPE: Floppy disk
COMPTER: IBM PC compatible
DEBRITING SYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patcettin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
SOFTMARE: Patcettin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
SOFTMARE: PATCHTON DATA:
PAPLICATION NUMBER: US.08/18/339
COMPANIE: PATCH NOW DATA:
PATCH DATE: 92-NOV-193
PATOR APPLICATION NUMBER: US.08/15/339
PATOR APPLICATION NUMBER: US.08/27,746
FILING DATE: 06-NG-193
PATOR APPLICATION NUMBER: US.08/27,746
FILING DATE: 06-SHAR.193
PATOR APPLICATION NUMBER: US.08/27,746
FILING DATE: 07-NG-193
PATOR APPLICATION NUMBER: US.07/926,666
APPLICATION NUMBER: US.07/926,666
FILING DATE: 07-NG-193
PATOR APPLICATION NUMBER: US.07/926,666
APPLICATION NUMBER: US.07/926,666
FILING DATE: 07-NG-193
PATOR APPLICATION NUMBER: US.07/926,666
APPLICATION NUMBER: US.08/927,746
APPLICATION NUMBER: US.08/927,746
APPLICATION NUMBER: US.08/927,746
APPLICATION NUMBER: US
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Result
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Maximum Match 100
Listing first 45
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            length: 0
length: 2000000000
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Match
4444444444488888663255531
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2227551156666488886662255531
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Gapop 10.0 ,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pir1:*
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pir3:*
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(c) 1993 - 2000 Comp
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12.086 Million cell updates/sec
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                                                                      circumsporozoite circum
                          hypothetical prot
circumsporozoite
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47	47.5	7.5	48	48	48	49	49	49	49	49.5	51	51	51	51	
37.4	37.4	37.4	37.8	37.8	37.8	38.6	38.6	38.6	38.6	39.0	40.2	40.2	40.2	40.2	
175	264	264	1714	778	778	802	485	429	387	993	395	387	387	386	
2 7	N	N	N	N	2	N	N	N	N	N	N	N	N	2	
G71480	H65058	F85927	E71609	C71944	A64656	T32448	A60610	A54504	в82891	B64695	A41156	C41156	D41156	A48571	
hypothetical prote	hypothetical prote	hypothetical prote	Ser/Thr protein ki		hypothetical prote	hypothetical prote	circumsporozoite p	circumsporozoite p	ferrichrome transp	type I restriction	circumsporozoite p	circumsporozoite p	circumsporozoite p	circumsporozoite p	

ALIGNMENTS

RESULT OZZQAF

circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate IMTM22) (Species: Diasmodium falciparum) (C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jun-2000 C;Accession: A03388 R;Dame, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W Science 225, 593-599, 1984 A;Title: Structure of the gene encoding the immunodominant surface antigen on the spo A;Reference number: A03388; MUID:84250215 A;Accession: A03388 A;Molecule type: DNA A;Residues: 1-412 <DAM> A;Cross-references: GB:K02194; NID:9160160; PIDN:AAA29524.1; PID:9160161 A;Experimental source: clone 7G8 C;Comment: Residues 1-16 are the probable signal sequence. C;Comment: Residues 1-16 are the probable signal sequence. C;Comment: Residues 1-16 are the probable signal sequence. C;Comment: There are 41 copies of a 4-residue repeating unit in the middle domain of C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology <THRI> A;Molecule type: DNA
A;Residues: 1-424
A;Residues: 1-424
A;Cross-references: GB:M19752; NID:g160216; PIDN:AAA29555.1; PID:g160217
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;348-402/Domain: thrombospondin type 1 repeat homology <THR1> R;del Portillo, H.A.; Nussenzweig, R.S.; Enea, V. Mol. Biochem. Parasitol. 24, 289-294, 1987 A;Title: Circumsporozoite gene of a Plasmodium falciparum strain from Thailand. A;Reference number: A54533; MUID:87315205 A;Accession: A54533 circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain C;Speckes: Plasmodium falciparum C;Date: 28-Oct.1994 #sequence_revision 28-Oct.1994 #text_change 09-Jun-2000 C;Accession: A54533 A; Status: preliminary B Query Match Best Local (Matches Query Match Best Local Similarity 368 1 KPKDELDYENDIEKKICKMEKCS KPKDELDYENDIEKKICKMEKCS 390 Similarity Conservative Conservative J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W 100 100 . 0%; .0%; 0; 0; 23 Score 127; DB 2; Pred. No. 8.2e-10; ; Mismatches 0; Score 127; DB 1 Pred. No. 8e-10; Mismatches +-0 Length 424; Length 412; Indels Indels 0, 0; Gaps Gaps T4, 0; 0

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MOI. Biochem. Parasitol. 22, 101-108, 1987
A). Title: Strain variation in the circumsporozoite protein gene (
A). Reference number: A54529; MUID:87115616
A). Accession: A54529
A). Status: preliminary; not compared with conceptual translation A; Molecule type: DNA
A). Molecule type: DNA
A). Residues: 1-442 < LOC>
A). Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1; PII
C). Superfamily: circumsporozoite protein: thrombospondin type 1 1
C). Keywords: tandem repeat
C). Keywords: tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           circumsporozoite protein - malaria parasite (Plasmodium falciparum) (strain Wellcome) C:Species: Plasmodium falciparum C:Date: 28-Oct-1994 #sequence_revision 28-Oct-1994 #text_change 09-Jun-2000 C:Accession: A54529
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A. Fitle: Circumsporozoite protein gene from plasmodium reichenowi, a chimpanzee A. Fitle: Circumsporozoite protein gene from plasmodium reichenowi, a chimpanzee A. Reference number: A39756; MUID:91201303
A. Rocession: A39756
A. Status: preliminary
A. Molecule type: DNA
A. Molecule type: DNA
A. Residues: 1-388 <LAL>
A. Residues: 1-388 <LAL>
A. Cross-references: GB. M60972; NID:9160228; PIDN:AAA29561.1; PID:9160229
A. Cross-references: GB. M60972; NID:9160228; PIDN:AAA29561.1; PID:9160229
C. Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology <FHR1>
F;312-366/Domain: thrombospondin type 1 repeat homology <FHR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                circumsporozoite protein - Plasmodium r
C;Species: Plasmodium reichenowi
C;Date: 14-Feb-1992 #sequence_revision
C;Accession: A39756
R;Lal, A.A.; Goldman, I.F.
R;Lal, A.A.; Goldman, I.F.
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circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate C;Spacies; Plasmodium falciparum) (C;Date: 07-Jun-1990 **sequence_revision 07-Jun-1990 **text_change 09-Jun-2000 C;Date: 07-Jun-1990 **sequence_revision 07-Jun-1990 **text_change 09-Jun-2000 C;Date: 07-Jun-1990 **A45527; I60657 C;Accession: S05428; A45527; I60657
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                                          R;Campbell, J.R.
Nucleic Acids Res. 17, 5854, 1989
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Best Local
A; Reference number:
       A; Title: DNA sequence of the A: Reference number: $05428; !
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91.3%;
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         gene encoding
MUID:89345189
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; Pred. No. 3.6e
2; Mismatches
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Pred. No. 2.2e-09;
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                                 Plasmodium falciparum malaria candidate
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A;Cross-references: GB:M22982; GB:J04650; NID:g160168; PIDN:AAA29527.1; PID:g160169 R;Lockyer, M.J.; Marsh, K.; Newbold, C.I. Mol. Biochem. Parasitol. 37, 275-280, 1989 A;Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cel A;Reference number: A60657; MUID:90114334 A;Accession: I60657
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A; Residues: 1-405 < CAM>
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A;Status: translation not shown
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A; Molecule type: DNA
A; Residues: 1-405 <CAS>
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A;Residues: 319-336,354-373 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;329-383/Domain: thrombospondin type 1 repeat homology <THR1>
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Mol. Biochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of plasmodium falciparum show extensive polymorphism A;Reference number: A60657; MUID:90114334
A;Accession: C60657
A;Status: preliminary; not compared with conceptual translation
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A; Residues: 1-38 <LOC>
C; Superfamily: circums
R; Lockyer, M.J.; Marsh, K.; Newbold, C.I.
R; Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Biochem. Parasitol. 37, 275-280, 1989
A; Title: Wild isolates of plasmodium falciparum show extensive |
A; Reference number: A60657; MUID:90114334
A; Accession: D60657
A; Status: preliminary; not compared with conceptual translation
                                                                                                                      C;Species: Plasmodium falciparum
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-Jun-2000
C;Accession: D60657
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95.7%;
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RESULT 8

£60657

Circumsporozoite protein - malaria parasite (Plasmodium falciparum)
C;Species: Plasmodium falciparum
C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change 09-C;Accession: £60657
R;Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Biochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falciparum show extensive polyn A;Reterence number: A60657; MUID:90114334
A;Accession: £60657
A;Status: preliminary; not compared with conceptual translation A;Molecule type: DNA
A;Residues: 1-38 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repe
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A38869
A38869
C:Species: Plasmodium falciparum
C:Species: Plasmodium falciparum
C:Accession: A38869
R:Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Biochem. Parasitol. 37, 275-280, 1989
A:Title; Wild isolates of Plasmodium falciparum shc A:Reference number: A60657; MUID:90114334
A:Accession: A38869
A:Status: preliminary; not compared with conceptual.
circumsporozoite protein - malaria parasite (Plasmodium C;Species: Plasmodium falciparum C:Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text C;Accession: B60657 R;Lockyer, M.J.; Marsh, K.; Newbold, C.I.
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A;Residues: 1-38 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
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A; Molecule type: DNA
A; Residues: 1-38 <LOC>
C; Superfamily: circumsporozoite
                                                                                                                                                                                                          R;Lockyer, M.J.; Marsh, K.; Newbold, C.I.
Mol. Blochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of Plasmodium falciparum show extensive polymorphism A;Reference number: A60657; MUID:90114334
A;Accession: B38869
                                                                                                                                                                                                                                                                                         circumsporozoite protein - malaria parasite (Plasmodium falcipar C;Species: Plasmodium falciparum C;Date: 03-Jun-1993 #sequence_revision 03-Jun-1993 #text_change C;Accession: B38869
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B38869
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A;Molecule type: DNA
A;Residues: 1-38 <LOC>
C;Superfamily: circumsporoz
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H60657
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C;Superfamily: circumsporozoite protein; thrombospondin type 1
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A; Residues: 1-38 <LOC>
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0.043;
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circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate 366-8) (fra C;Species; Plasmodium falciparum) c;Date: 03-Jun-193 #sequence_revision 03-Jun-1993 #text_change 09-Jun-2000 C;Accession: G60657
R;Lockyer, M.J; Marsh, K.; Newbold, C.I.
MOI. Biochem. Parasitol. 37, 275-280, 1989
A;Title: Wild isolates of plasmodium falciparum show extensive polymorphism in T cell ef A;Reference number: A60657; MUID:90114334
A;Accession: G60657
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: DNA
A;Residues: 1-38 <-COC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
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A; Molecule type: DNA
A; Residues: 1-161 CDEL>
A; Cross references: GB:M17802; GB:M17803; GB:M17806
MOI. Biochem. Parasitol. 37, 275-280, 1989
A; Title: Wild isolates of Plasmodium falciparum show extensive polymorphism in T cell ep.
A; Reference number: A60657; MUID:90114334
A; Recession: A60657
A; Status: preliminary; not compared with conceptual translation
A; Molecule type: DNA
A; Residues: 152-189 <LCC>
C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
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A;Molecule type: DNA
A;Residues: 1-38 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
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Listing first 45 summaries
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P13814;
01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
Plasmodlum falciparum (isolate t4 / Thailand).
Eukaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE-87315205; PubMed=3306373; del Portillo H.A., Nussenzweig R.S., En "Circumsporozoite gene of a Plasmodium Thailand.";
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PIR; A54533; A54533.
InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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                      01-AUG-1988 (Rel. 08, Created)
01-AUG-1988 (Rel. 08, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CIRCUMSPORZOITE PROTEIN PRECURSOR (CS).
Plasmodium falciparum (isolate Wellcome).
Eukaryota: Alveolata: Apicomplexa; Haemospori
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WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                 Haemosporida;
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SEQUENCE FROM N.A.
MEDLINE-87115616; PubMed=3543671;
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SEQUENCE
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01-AUG-1992 (Rel. 23, Last sequence
20-AUG-2001 (Rel. 40, Last annotatic CIRCUMSPOROZOITE PROTEIN PRECURSOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Malaria;
                                                                                                Lal A.A., Goldman I.F.;

"Circumsporozoite protein gene from plasmodium reichenowi, a "Circumsporozoite protein gene from plasmodium reichenowi, a chimpanzee malaria parasite evolutionarily related to the human malaria parasite plasmodium falciparum.";

J. Biol. Chem. 266:6686-6689(1991).

-i- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT

-i- FUNCTION: THE CIRCUMSPOROZOITE (THE INFECTIVE STAGE OF THE SURFACE ANTIGEN ON THE SPOROZOITE) FROM THE MOSQUITO TO THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium reichenowi.
Eukaryota; Alveolata; Apicomplexa;
                                                                                                                                                                                                                                                                                                      MEDLINE=91201303;
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=5854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAS WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 KPKDELDYENDIEKKICKMEKCS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VERTEBRATE HOST)
                                                     MISCELLANEOUS:
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PF00090; tsp_1; 1.
PF00090; tsp_1; 1.
     ANCHORING THE PROTEIN TO THE CELL MEMBRANE. WOULD BE THE SURFACE ANTIGEN OF THE ORGANIS
                                                                                   VERTEBRATE HOST)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SM00209; TSP1;
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22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               130
442 AA;
                                                                                                                                                                                                                                                                                 Goldman I.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schwarz
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                              PubMed=2016283;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            442 CIRCUMSPOROZOITE PROTEIN.
320 47 X 4 AA TANDEM REPEATS
47402 MW; BD57A9A152B85E03 CRC64;
                                             THE C-TERMINAL REGION IS PROBABLY USED FOR SECTION TO THE CELL MEMBRANE. THE REPEAT SE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97.6%;
95.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Last sequence up
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Pred.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 124;
No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                       Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (CS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
1.6e-09;
0;
                  ORGANISM
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                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium.
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                                                SEQUENCES
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Best Local S
Matches 21
SEQUENCE FROM N.A.

MEDLINE-89364998; PubMed-2671723;
Caspers P., Gentz R., Matile H., Pink J.R., Si:
"The circumsporozoite protein gene from NF54,
"The circumsporozoite circumstalis.";
I isolate used in malaria vaccine trialis.";
L Mol. Biochem. Parasitol. 35:185-190(1989).
C -!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CSP_PLAFO PT; 3
P19597; O25798;
01-FEB-1991 (Rel. 17, Created) ...
30-MAY-2000 (Rel. 39, Last sequence up 20-AUG-2001 (Rel. 40, Last annotation of the company of the compa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DOMAIN
SEQUENCE
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InterPro; IPR000884; TSP1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the European Bioinformatics Institute. There are no restrictions on use by non-profit institutions as long as its content is in no modified and this statement is not removed. Usage by and for commen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This
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Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS). Plasmodium falciparum (isolate NF54).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thomas A.W., Bagar Hackett C.S.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 infectivity of a
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=5843;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   *Plasmodium falciparum:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       344
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                                                                                                                                                                                                                                                                                                                                                                                          Parasitol.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sporozoite; Repeat;
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388 AA;
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267 6
42245 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        S., Cochran M.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17:5854-5854(1989)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    J.F., Herrington D.A., Murphy J.R., Clyde D.F., S., Cochran M.A., Thanassi J., Levine M.M.,
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91.3%;
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line.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE=87102878; PubMed=3802196;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   CSP_PLACL P08675;
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                                                                                                                                                                                                                                                                                            Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W., Nussenzweig R.S., Enea V.;
                                                                                                                                                                                                                                                                                                                                                                        Plasmodium cynomolgi (strain London)
Eukaryota; Alveolata; Apicomplexa; F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REPEAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPEAT
                                                                                                                                                                                                                                                                                                                    MEDLINE=87102878; PubMed=3802196;
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      01-JAN-1988
                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=5831;
                         EMBL; M15101; AAA29537.1; - PIR; A26255; OZZQAL.
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                                                                         use by non-profit institumodified and this statement entities requires a license
                                                                                                                            between
                                                                                                                                                                                                                                                                   "The circumsporozoite gene of the Plasmodium Cell 48:311-319(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               335
            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 KPKDELDYENDIEKKICKMEKCS
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                                                                                                                                                              MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEGMOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                           s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               KKPEELDV-NDLETEVCTMDKCA
                                                                                                                                                                                                                   VERTEBRATE HOST)
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IPR000884;
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attement is not removed. Usage by an
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19 PROBABLE.

778 CIRCUMSPOROZOITE PROTEIN.

92 10.5 X 9 AA REPEATS.

92 10.5 X 9 AA TANDEM REPEATS.
                                                                                                   rmatics Institute. There are no rest institutions as long as its content
             Crcmsprzoite
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P08673;
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01-JAN-1988
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SIGNAL
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01-JAN-1988 (Rel. 06, Last sequence updat
20-AUG-2001 (Rel. 40, Last annotation upc
CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS).
Plasmodium cynomolgi (strain Ceylon).
Eukaryota; Alveolata; Apicomplexa; Haemos
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PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "The circumsporozoite gene of the Plasmodium cynomolgi complex."; Cell 48:311-319(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Galinski M.R., Arnot D.E., Cochrane A.H., Barnwell J.W
                                                                SIGNAL
CHAIN
                                                                                                                                                                                                                                                                                                modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                           between
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A. MEDLINE=87102878; PubMed=3802196;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=5829;
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                                                                                                                                                                                                                                                         EMBL; M15103; AAA29533.1; -.
    SEQUENCE
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SMART; SM00209; TSP1;
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InterPro; IPR000884; TSP1.
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                                                DOMAIN
                                                                                                           Malaria;
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ANCHORING THE PROTEIN TO THE CELL MEMBRANE. T
WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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6; Mismatches
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Q-A-G-A-G.
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18 X 6 AA TANDEM REPEATS
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17 X 9 AA TANDEM
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                      CSP_PLACM
P08676;
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P08674;
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Eukaryota: Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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01-JAN-1988 (Rel.
20-AUG-2001 (Rel.
 01-JAN-1988
01-FEB-1996
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InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
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ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE
WOULD BE THE SUPPACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MISCELLANEOUS: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE VERTEBRATE HOST).
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SM00209; TSP1; 1
                                                                                                                                       l Similarity 47.1
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98
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Pred. No. 0.45
6; Mismatches
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CIRCUMSPOROZOITE PROTEIN.
17 X 11 AA TANDEM REPEATS
A-A-G-G-G-G-N.
57D666268238503E CRC64;
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Interp
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01-JAN-1988
20-AUG-2001
                                                        Eichinger D.J., Arnot D.E., Tam J.P., Nussenzweig "Circumsporozoite protein of Plasmodium berghei: identification of the immunodominant epitopes."; Mol. Cell. Biol. 6:3965-3972(1986).
                                                                                                                                                                                                                                                                             20-AUG-2001 (Rel. CIRCUMSPOROZOITE |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-sib.ch).
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                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                     Plasmodium berghei.
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This
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Eukaryota; Alveolata; Apicomplexa; Haemospo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Last annotation CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS
                                                                                                                         MEDLINE-87089740; PubMed-2432395;
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[1]
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InterPro; IPR000884; TSP1.
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COLI. BIO1. 6:3955-3972(1986).
FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THI MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THI
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ANCHORING THE PROTEIN TO THE CELL MEMBRANE:
WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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3; CRCMSPRZOITE.
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Pred. No. 0.
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54 X 4 AA TANDEM REPEATS;
8F46CDD8A1B4EFF4 CRC64;
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pROSITE; PS50092; TSP1; 1.
Malaria; Sporozoite; Repeat;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  CSP_PLABA STANDARD; PRT; 347 AA. p23093; p23093; (Rel. 20, Created) 01-NOV-1991 (Rel. 20, Last sequence update) 20-AUG-2001 (Rel. 40, Last annotation update) CIRCUMSPOROZOITE PROTEIN PRECURSOR (CS). Plasmodium berghei (strain Anka). Plasmodium berghei (strain Anka). Bukaryota; Alveolata; Apicomplexa; Haemosporida; Enkaryota; Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SIGNAL
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InterPro; IPR000884; TSP1.
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use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                  Lockyer M.J., Davies C.S., Suhrbier A., Sinden R.E.;
"Nucleotide sequence of the Plasmodium berghel circumsporozoite
protein gene from the ANKA clone 2.34L.";
nucleic Acids Res. 18:376-376(199).

-i- FUNCTION: THE CINCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
MEDLINE-90221834; PubMed=2183186;
                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=5823;
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                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
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MISCELLANEOUS: THE C-TERMINAL REGION IS PROBA
MISCELLANEOUS: THE COTEIN TO THE CELL MEMBRANE. T
ANCHORING THE PROTEIN TO THE CELL MEMBRANE. T
WOULD BE THE SURFACE ANTICEN OF THE ORGANISM.
SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
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PROBABLE.
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13 X 8 AA TANDEM REPEATS.
16 X 2 AA TANDEM REPEATS OF; E8068A6D11D9551B CRC64;
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                                                                                                                                                                                                      REGION IS PROBABLY USED FOR
CELL MEMBRANE. THE REPEAT SEQUENCES
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L outstation -
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RESULT
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Best Local S
Matches 12
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CSP_PLAYO STANUANA,
P06914;
P01-JAN-1988 (Rel. 06, Created)
P01-JAN-1988 (Rel. 06, Last sequence used to the control of t
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SEQUENCE
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InterPro; IPR003067; Crcmsprzoite.
InterPro; IPR000884; TSP1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Malaria; Sporozoite;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium berghei yoc
Eukaryota; Alveolata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Structure of the gene encoding the plasmodium yoelii. A rodent model sporozoite vaccines."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A
MEDLINE=87137555;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE OF 1-140 AND 260-367 FROM N.A. MEDLINE-88232798; PubMed-3287156; del la Cruz V.F., Lal A.A., McCutchan T.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=5862;
                                                                                                                                                                                                                                                                                                                                                                                                                                Mol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           de la Cruz V.F., Lal A.A., McCutchan T.F.; "Variation among circumsporozoite protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lal A.A., de la
McCutchan T.F.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   304
                                                                                  use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malarias.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Biol, Chem. 262:2937-2940(1987)
                                                                                                                                                                                                                                                                 MISCELLANEOUS: THE C-TERMINAL REGION IS PROBABLY USED FOR ANCHORING THE PROTEIN TO THE CELL MEMBRANE. THE REPEAT SEX WOULD BE THE SURFACE ANTIGEN OF THE ORGANISM. SIMILARITY: CONTAINS 1 TSP TYPE-1 DOMAIN.
                                                                                                                                                                                                                                                                                                                                                                                Biochem. Parasitol. 28:31-38(1988).
EUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOM SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KKAEDLTLE-DIDTEICKMDKCS
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SM00209; TSP1;
  J02695;
M18821;
M22698;
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12; Conserv
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347
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93
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    AAA29558.1; -.
AAA29559.1; -.
AAA29560.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pubMed=3102479;
ruz V.F., Welsh J.A., Charoenvit Y., Maloy W.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      06, Created)
06, Last sequence update)
40, Last annotation updat
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204
247
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Pred.
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13 X 8 AA REPEATS.
17 X 2 AA REPEATS OF P-Q.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Signal.
POTENTIAL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                            THE IMMUNODOMINANT
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CRC64;
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F
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MRL outstation -
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                                                                                                                                                                                                                       outstation
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RESULT 14
3HAO_YEAST
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Best L
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SEQUENCE
                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation—the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                Kucharczyk R., Zagulski M., Rytka J., Herbert C.J.;
"The yeast gene YJR025c encodes a 3-hydroxyanthranilic acid dioxygenase and is involved in nicotinic acid biosynthesis.";
FEBS Lett. 424:127-130(1998).
-I- CATALYTIC ACTIVITY: 3-HYDROXYANTHRANILATE + O(2) = 2-AMING
                                                                                                                                                                                                                                                                                                                                                                                   Zagulski M., Babinska B., Gromadka R., Migdalski A., Rytka J., Sulicka J., Herbert C.J.; Sulicka J., Herbert C.J.; "The sequence of 24.3 kb from chromosome X reveals five complete reading frames, all of which correspond to new genes, and a tande insertion of a Tyl transposon."; Yeast 11:1179-1186(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetales; Saccharomycetaceae; Saccharomyces
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-FEB-1996 (Rel.
01-FEB-1996 (Rel.
15-JUL-1999 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DOMAIN
             EMBL; Z49525; CAA89550.1; -. EMBL; X87297; CAA60720.1; -. SGD; S0003786; BNA1.
                                                                                                                                                                                                     -!- COFACTOR: FERROUS ION.
-!- PATHWAY: INVOLVED IN NICOTINIC AC-
-!- SIMILARITY: STRONG, TO MAMMALIAN
                                                                                                                                                                                                                                                                                                                                      CHARACTERIZATION.
MEDLINE-98198537; PubMed-9539135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
3-HYDROXYANTHRANILATE 3,4-DIOXYGENASE (EC 1.13.11.6) (3-HAO)
(3-HYDROXYANTHRANILIC ACID DIOXYGENASE) (3-HYDROXYANTHRANILATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CHAIN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Malaria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=96109930; PubMed=8619316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HAO_YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          324 KQPENLTLE-DIDTEICKMDKCS 345
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                                                                                                                                                                                                                                                     CARBOXYMUCONATE SEMIALDEHYDE.
                                                                                                                                                                                           DIOXYGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; PR01303; CRCMS
SM00209; TSP1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity 52.
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139
229
367
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3; CRCMSPRZOITE.
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Dioxygenase;
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228 J
260 E
38888 MW;
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Pred. No. 1.4;
4; Mismatches
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01-JAN-1990
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-!- FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THIS MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE MOSQUITO THE MALARIA PARASITE THAT MALARIA PAR
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MCCUtchan T.F., Lal A.A., de la Cruz V.F.,
Charoenvit Y., Beaudoin R.L., Guerry P., W
"Hockmeyer W.T., Collins W.E., Wirth D.;
"Sequence of the immunodominant epitope fo
sporozoites of Plasmodium vivax.";
Science 230:1381-1383(1985).
                                                                                                                                                                                                                    Sporozoite; Malaria; Repeat.
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DOMAIN 63 243
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NCBI_TaxID=5856;
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ALIGNMENTS

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Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 23; Conservative 0
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InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
SMARP; SM00209; TSP1; 1.
NON_TER 1 1
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                                                                                                                                                                                                                                                                                             "Sequence variation in the non-repeat region of the Plasmodium falciparum glutamate rich protein (GLURP) from Brazil, Senegale Burmese field isolates and from laboratory strains."; Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJZ69941; CAB64167-1; ".

InterPro; IPR000884. "cn"
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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de Stricker K., Vuust J.,
(TrEMBLrel. 13, Created)
(TrEMBLrel. 13, Last sequence up
(TrEMBLrel. 17, Last annotation
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                                                                         0;
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                                                                                                                                                                A3283B70CEE50FDE CRC64;
                                                                                        Score 127; DB 5;
Pred. No. 1.1e-09;
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Query Match
Best Local Similarity
Matches 23; Conserv
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01-MAY-2000
01-JUN-2001
                                                                                                                                                                                        "Sequence variation in the non-repeat region of the Plasmodium "Sequence variation in the non-repeat region of the Plasmodium falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, Burmese field isolates and from laboratory strains. ";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJZ69961; CAB64180.1; ".
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_l; 1.
PRINTS; PR01301. Provent
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Burmeted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

EMBL; AJ26957; CAB64237.1;

InterPro; IPR003084; TSP1.

InterPro; IPR003087; Crcmsprzoite.

Pfam; PF00099; tsp1; 1.

PRINTS; PR01303; CRCMSPRZOITE.

SMART; SM00209; TSP1; 1.
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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Eukaryota;
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01-MAY-2001 (TrEMBLrel. 13,
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SEQUENCE
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PR01303; CMC...
                                                                                                                                                                           SM00209;
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(OTTE PROTEIN (FRACMENT).
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No. 1.1e-09;
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01-MAY-2000
01-MAY-2000
01-JUN-2001
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Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ269969; CAB64188.1; -.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp 1: 1
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Eukaryota; Alveolata;
NCBI_TaxID=5833;
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01-JUN-2001 (TrEMBLrel. 17, Last an
CIRCUMSPOROZOITE PROTEIN (FRAGMENT)
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SEQUENCE
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                                                                                                                                                                                                      STRAIN-B1896;
de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;
Sequence variation in the non-repeat region of the Plasmodium
'Sequence variation in the non-repeat (GLURP) from Brazil, Senegalese,
falciparum glutamate rich protein (GLURP) from Brazil, Senegalese,
falciparum flutamate and from laboratory Strains."
Burmese field isolates and from laboratory Strains."
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01-JUN-2001
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                                                             Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL: AJ269978; CAB64197.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
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Eukaryota; Alveolata;
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50 KPKDELDYENDIEKKICKMEKCS
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                                               SMART; SM00209; TSP1;
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23; Conservative
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ZOITE PROTEIN (FRAGMENT).
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13, Last sequence update)
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Pred. No. 1.1e-09;
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"Sequence variation in the non-repeat region of the Plasmod
T falciparum glutamate rich protein (GLURP) from Brazil, Sene
T Burmese field isolates and from laboratory strains."

L Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

R EMBL; AJ269955; CAB642211; -.

R EMBL; AJ269958; CAB64239.1; -.

R EMBL; AJ269959; CAB642211; -.

R EMBL; AJ269956; CAB64221.1; -.

R EMBL; AJ269956; CAB6421.1; -.

R EMBL; AJ269956; CAB64221.1; -.

R EMBL; AJ269956; CAB64239.1; -.

R EMBL; AJ2699
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Eukaryota; Alveol
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9TVP9;
01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                               01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
STRAIN=M0, M6, M7, AND M1;
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NCBI_TaxID=5833;
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               SEQUENCE FROM N.A.
STRAIN-B1893, B1804, B1853, B1870, B1872, B1881,
de Stricker K., Vuust J., Jepsen S., Oeuvray C.,
"Sequence variation in the non-repeat region of t
falciparum glutamate rich protein (GLURP) from BJ
                                                                                                                                                                                                                                                                                                Q9TVN9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SMART; SM00209; TSP1;
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23; Conserv
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23; Conserv
                                                                                                                                              falciparum.
Alveolata;
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Milarity 100.
Conservative
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9074 MW;
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                                                                                                                                            Apicomplexa;
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13,
17,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A8F40C90DB1C033E CRC64;
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Pred. No. 1.1
); Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 127; DB 5;
Pred. No. 1.1e-09;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       e 127; DB 5;
. No. 1.1e-09;
smatches 0;
                                                                                                                                              Haemosporida;
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y C., Thersen ...
on of the Plasmodium
from Brazil, Senegale
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                                                     AND B1882;
Theisen M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 80;
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                                                                                                                                              Plasmodium
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                 Senegalese,
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Q27425 ID . Q: AC Q:

Q27425; Q27425;

PRELIMINARY;

PRT;

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RESULT OPTWAY

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Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local S
Matches 23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Burmese field isolates and from laboratory strains.";
Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ69977; CAB64196.1; -.
EMBL; AJZ69971; CAB64190.1; -.
EMBL; AJZ69972; CAB64191.1; -.
EMBL; AJZ69973; CAB64191.1; -.
EMBL; AJZ69974; CAB64191.1; -.
EMBL; AJZ69975; CAB64191.1; -.
EMBL; AJZ69976; CAB64193.1; -.
EMBL; AJZ69976; CAB64195.1; -.
EMBL; AJZ69976; CAB64195.1; -.
InterPro; IPR003084; TSP1.
InterPro; IPR003084; TSP1.
InterPro; IPR030367; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-MAY-2000
01-MAY-2000
01-JUN-2001
                                                                                                                                                                                                                                                    Pfam; PF
PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. STRAIN-815, 947, AND 808; MEDLINE-95077069; PubMed-7985759;
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EMBL; M83153; AAA29566.1; -.

EMBL; M83171; AAA29549.1; -.

EMBL; M83151; AAA29564.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                      Jongwutiwes S., Tanabe K., Hughes M.K., Kanbara "Allelic variation in the circumsporozoite prote falciparum from Thai field isolates.";
                                                                                                                                                                                                                                                    InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CIRCUMSPOROZOITE
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                                                                                                                                                                                         SEQUENCE
                                                                                                                                                                                                                                     SMART;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium
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71
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  KPKDELDYENDIEKKICKMEKCS
                                                                                                                                                                                                                                ; PR01303; CRCM;
SM00209; TSP1;
                                                                                th 100 similarity 100 23; Conservative
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23; Conserv
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Alveolata; Apicomplexa;
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9074 MW;
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                                                                                Score 127; D
Pred. No. 1.5
0; Mismatches
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Pred.
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                                                                                     2 127; DE NO. 1.5e-09;
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. No. 1.1e-09;
smatches 0;
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                                                                                                                        Length 115;
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Best Loc
Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum
Eukaryota; Alveolata;
NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CSP.
Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1996 (TrEMBLrel 01, 01-NOV-1996 (TrEMBLrel 01, 01-JUN-2001 (TrEMBLrel 17, CIRCUMSPOROZOITE PROTEIN.
                                                                                                                                                                                                                                                     Q99256;
01-NOV-1996
01-NOV-1996
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE-84250215; PubMed-6204383;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jongwutiwes S., Tanabe K., Kanbara H.; Submitted (MAR-1992) to the EMBL/GenBank/DDBJ EMBL; M83169; AAA29547.1; -. EMBL; M83149; AAA29562.1; -. InterPro; IPR003084; TSP1. InterPro; IPR003067; Crcmsprzoite.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN=844;
la Cruz V.F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM
                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
CIRCUMSPOROZOITE PROTEIN (CS) PRECURSOR, VARIANT 2 (FRAGMENT).
Plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE
SMART; SM00209; TSP1; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-844
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Submitted (MAR-1992)
                                                                                                                                                                                                                                                                                                       Q99256
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                      protein gene.";
Mol. Biochem. Parasitol. 45:179-182(1991).

Mol. Biochem. Parasitol. 45:179-182(1991).

-I. FUNCTION: THE CIRCUMSPOROZOITE PROTEIN IS THE IMMUNODOMINANT
SURFACE ANTIGEN ON THE SPOROZOITE (THE INFECTIVE STAGE OF THE
MALARIA PARASITE THAT IS TRANSMITTED FROM THE MOSQUITO TO THE
                                                                                                                                                               MEDLINE=91270295;
                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                  NCBI_TaxID=5833;
                                                                                                                                                                                                                 Eukaryota;
                                                                                                                                      "Clonal variation in the
                                                                                                                                                   Lockyer
                                                                                                                                                                                                                                                                                                                                                                      380
                                                                                                                                                                                                                                                                                                                                                                                                                                  y Match
Local S
                                                                                                                                                                                                                                                                                                                                                                                  1 KPKDELDYENDIEKKICKMEKCS
VERTEBRALL
MISCELLANBOUS: THE CALCHORING THE PROTEIN TO THE CANCHORING THE SURFACE ANTIGEN
AAA63422.1; -
                                                                                                                                                                                                                                                                                                                                                                      KPKDELDYENDIEKKICKMEKCS 402
                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                                                                                                                                                                                                                 Alveolata; Apicomplexa; Haemosporida;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                  PubMed=2052038;
                                  THE C-TERMINAL REGION IS PROPROTEIN TO THE CELL MEMBRANE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       45592 MW;
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Submitted (MAR-1992) to the EM
EMBL; M83155; AAA29566.1; -
EMBL; M83170; AAA29565.1; -
EMBL; M83152; AAA29565.1; -
EMBL; M83158; AAA29571.1; -
EMBL; M83168; AAA29574.1; -
EMBL; M83168; AAA29546.1; -
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PRINTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Dame J.B., Williams J.L., McCutchan T.F., Hockmeyer W.T., Maloy W.L., Haynes J.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=84250215; PubMed=6204383;
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NCBI_TaxID=5833;
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SMART; SM00209; TSP1;
SEQUENCE 432 AA; 4
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InterPro; IPRO03067; Crcmsprzoite
Pfam; PP00090; tsp_1; 1.
PRINTS; PR01303; CRCMSPRZOITE.
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    Score 127; DB 5;
Pred. No. 5.1e-09;
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Schneider I., Roberts D.
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Mol. Biochem. Parasitol. 0.0-0(0).
EMBL; M83165; AAA29543.1; -.
InterPro; IPR000884; TSP1.
InterPro; IPR003067; Crcmsprzoite.
Pfam; PF00090; tsp_1; 1.
PRLNTS; PR01303; CRCMSPRZOITE.
SMART; SM00209; TSP1; 1.
SEQUENCE 432 AA; 46385 MW; 2CE8D
de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theise "Sequence variation in the non-repeat region of the platfalciparum glutamate rich protein (GLURP) from Brazil, Burmese field isolates and from laboratory strains.";
                                                                                                                                    01-MAY-2000 (TrEMBLrel. 13,
01-MAY-2000 (TrEMBLrel. 13,
01-JUN-2001 (TrEMBLrel. 17,
CIRCUMSPOROZOITE PROTEIN (FI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-84250215; PubMed-6204383;
Dame J.B., Williams J.L., McCutchan T.F., Weber J.L., Wirtz R.A.,
Hockmeyer W.T., Maloy W.L., Haynes J.D., Schneider I., Roberts D.,
Sanders G.S., Reddy P.E., Diggs C.L., Miller L.H.;
"Structure of the gene encoding the immunodominant surface antigen
the sporzozite of the human malaria parasite Plasmodium falciparum.
Science 225:593-599(1984).
                                                                                    Plasmodium falciparum (isolate K1 / Thailand). Eukaryota; Alveolata; Apicomplexa; Haemosporida; NCBI_TaxID=5839;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum.
Eukaryota; Alveolata;
NCBI_TaxID=5833;
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Pred. No. 5.1
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No. 5.1e-09;
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01-MAY-2000 (TrEM)
01-MAY-2000 (TrEM)
01-JUN-2001 (TrEM)
CIRCUMSPOROZOITE
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SEQUENCE
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PRINTS; PR0133; CRCMSPRZOITE.
PROSITE; PS50092; TSP1; 1.
SMART; SM00209; TSP1; 1.
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PRINTS; PR01303; CRCMSPRZOITE
SMART; SM00209; TSP1; 1.
                                                                                                                                                                                                                                                  Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases. EMBL; AJ269948; CAB64173.1; -. InterPro; IPR0003067; Crcmsprzoite.
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de Stricker K., Vuust
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InterPro; IPR003067; Crcmsprzoite
Eukaryota;
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Rd de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

Rd de Stricker K., Vuust J., Jepsen S., Oeuvray C., Theisen M.;

RT Sequence variation in the non-repeat region of the Plasmodium

RT falciparum glutamate rich protein (GLURP) from Brazil, Senegalese, and

RT Burmese field isolates and from laboratory strains.";

RT Burmese field isolates and from laboratory strains.";

RS Submitted (SEP-1999) to the EMBL/GenBank/DDBJ databases.

RL EMBL; AJZ69951; CAB64176.1; -

DR InterPro; IPR000884; TSP1.

DR InterPro; IPR003067; Cromsprzoite.

PFAnn; PF00090; tsp_1; 1.

DR PFAnn; PF00090; tsp_1; 1.

DR SMART; SM00209; TSP1; 1.

PR NON_TER 80 80

SQ SEQUENCE 80 AA; 9032 MW; ADED6F0E266AD98E CRC64;
Search completed: January 29, 2002, 11:12:10 Job time: 766 sec
                                                                                         В
                                                                                                                                                            Query Match 97.6%; Score 124; DB 5; Length 80; Best Local Similarity 95.7%; Pred. No. 2.7e-09; Matches 22; Conservative 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN=L1;
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AAP90064	AAR65375	AAY49259	AAY49255	AAY49254	AAY49253	AAY49252	AAY99033	AAB07288	AAP93560	AAG63516	AAR83570	AAR62715	AAR82077	AAB98457	AAB84447	AAG89366	AAG88269	AAG84517	AAG62428	AAB99706	AAY58777	AAY54553	AAY80071	AAY23252	AAW35440	AAW05612	AAR70912	AAR75955	AAR78920 .	AAR82586	AAP91504	AAP80835	AAR37797	
Antigenic protein	Helper T cell epit	+ T cell	N19 polyepitope ca		N10 polyepitope ca	polyepitop	HLA class II bindi	m	Plasmodium berghei	eptide which	IgE CH4 region con	LHRH-containing im	Malaria CST3 prote	Plasmodium falcipa	Ę,	Plasmodium falcipa			Plasmodium falcipa	Plasmodium falcipa	16	T helper cell (Th)	Pathogen derived T	Peptide derived fr	T-cell stimulatory	Circumsporozoite h	Malaria circumspor	P. falciparum CS p	Malaria circumspor	alc	e of modi	uence encoded	RTS* protein. Syn	

ALIGNMENTS

AAY70283 standard; peptide;

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06-JUN-2000 AAY70283;

(first entry)

Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein: CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody. (NAIM-) WPI; 2000-237654/20. Lal AA, Shi YP, Hasnain 21-AUG-1998; 02-MAR-2000. WO200011179-A1. Plasmodium falciparum Plasmodium falciparum CSP antigenic epitope, P594. 19-AUG-1999; NAT INST IMMUNOLOGY.
US DEPT HEALTH & HUMAN SERVICES. 98US-0097703 99WO-US18869

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RESULT AAR13175 ID AAR13175 ID AAR13175 AAR13175 AAR1 AC AAR1 
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Matches 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle \,
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                           19-JUN-1991.
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hybrid; influenza virus; non-structural protein 1; fusion.
                                                                            EP432965-A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      virus
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/note= "Influenza virus nonstructural protein 1"
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89..19:
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inal AAS"
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_____signal sequence"
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                                                                                                                                                                                                                                                                                                                                                                  /label= artifact
                                                                                                                                                                                                                                                                                     /label= AAs 19-123 of CS protein
                                                                                                                                                                                                                                                                                                                                                                                                                   /label= synthetic linker
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Pred. No. 4.4e-10;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein i (NS1), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1 (NS1_81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking regionless the 18 AA signal region, which in turn is fused to DNA encoding Region II-contg. flanking regionless the 18 AA signal region is designated RLIGelta9. The Pro residue separating the Asp (at the C-terminal for the linker) from RLIGelta9 is an artifact of a filled in BamHI in the Asp (at the C-terminal Asis This CS (as in State of the linker) from RLIGelta9 is an artifact of a filled in BamHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         polypeptide comprising immunogenic determinants from P - for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM.
(USSA ) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST
                                                                                                                                                                   Key
Domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1991-179771/25.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                         AAR07945 standard; protein; 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  See also AAR12306-R12311 and AAR13176-R13179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 1; Page 7; 18pp; English.
            01-MAY-1990;
                                                                                                    Domain
                                                                                                                              Domain
                                                                                                                                                                                                           Plasmodium
                                                                                                                                                                                                                                    Malaria; vaccine
                                                                                                                                                                                                                                                             NS181RLFAuth
                                                                                                                                                                                                                                                                                        22-FEB-1991
                                                                                                                                                                                                                                                                                                                 AAR07945;
                                     22-NOV-1990
                                                               EP398540-A.
                                                                                                                                                                                                                                                                                                                                                                                                        1 DIEKKICKMEKCSSVFNVVNS
                                                                                                                                                                                                                                                                                                                                                                   ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The peptide can be used in a vaccine for protection against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          309
                                                                                                                                                                                                          falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                             plasmid product
                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ΑA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        89US-0447746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 90EP-0313257
            90EP-0304720
                                                                                                                              89..193
                                                                                                                                         /label= NS181 protein
/note= "from plasmid p
                                                                                                                                                                                 location/Qualifiers
                                                                                                                label = Fragment of circumsporozite protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hollingdale MR
                                                                                        Fragment of circumsporozite protein
                                                                                                                                                                                                                                                                                                                                                                                                            295
                                                                                                                                                                                                                                                                                                                                                                                                                                    21
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 109; DB 12;
Pred. No. 7.1e-09;
Pred. No. 7.1e-09;
                                                                                                                                                                                                                                                                                                                                           AA
                                                                                                                                            n fragment
pMG-1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 309;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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PROXXE PROXXE PROPERTY OF THE FORTH 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                  Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The product is useful in preparation of vaccines for treatment and prophylaxis of plasmodium sporozite infection. It may be easily produced in large pure quantities from a transformed E.coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New polypeptide used in malaria vaccine - comprises immunoge determinants from 1st and 2nd flanking regions of plasmodium surface protein and intermediate repeat domain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 11-12;
06-DEC-1990;
                                 19-JUN-1991
                                                                                                                               Region
                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                  Region
                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                   Peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
hybrid; influenza virus; non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NS1_81-RLfAuth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR13176;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAR13176 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ06580.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1990-350299/47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   03-MAY-1989;
                                                              EP432965-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                       Influenza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (SMIK ) SMITHKLINE BEECHAM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           system
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            319 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   89US-0346863
90EP-0313257.
                                                                                                                                                                                                                                /note= "
89..193
/label=
                                                                                                                                                                                                                                                                                                                                                                                                                                     (A/PR/8/34).
                                                                                                                                                                                                                                                                                                                                   /note= "Influenza virus nonstructural protein 1" 82..87
                                                                                                                               /note="see comments"
195..319
                                                                                                                                                                                 194
                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                                 /label= artifact
/note= "see comments"
                                                                                                 /note=
                                                                                                                                                                /label= artifact
                                                                                                                                                                                                                                                                                                                    /label= synthetic linker
                                                                                                                                                                                                                                                                                                                                                                   /label= N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          24pp; English.
                                                                                              "Region II flanking region"
                                                                                                                                                                                                               "Region
                                                                                                                                                                                               "Region 1 contg.
signal sequence"
                                                                                                                                                                                                                              AAs 19-123 of CS protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 109; DB 11;
Pred. No. 7.4e-09;
: Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A
                                                                                                                                                                                                             flanking region less
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 319;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 QΥ
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AAR13177
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NSI), [Baze et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NSI (NSI_81) is linked via a synthetic sequence to DNA encoding Region I contg. flanking regionless the 18 AA signal region, which in the contg. flanking regionless the 18 As signal region, which in the contg. flanking regionless the 18 As signal region, which in the contg. flanking region II-contg. flanking region for the Asp (at the C-terminal of the linker) from RLfAuth is an article fact of a filled in BamHI site; the Gly separating Region I and C Region II-contg. CS flanking regions is an artifact of a synthetic PokI/TthIII I linker. The peptide can be used in a vaccine for the contraction against malaria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gross MS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (SMIK )
Region
                                                                   Region
                                                                                                                                                                                                                                                                                                                         Immunogenic determinant;
hybrid; influenza virus;
                                                                                                                                                                                                                                                                                                                                                                                            NS1_81-RLfAuth + (NANP)2.
                                                                                                                                                                                                                                                                                                                                                                                                                                          29-AUG-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR13177;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAR13177 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     See also AAR12306-R12311 and AAR13175-R13179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 2; Page 10; 18pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Polypeptide comprising immunogenic determinants from P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (USSA ) US SEC OF THE ARMY. (BIOM-) BIOMEDICAL RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 08-DEC-1989;
                                                                                                                Peptide
                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                            Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The complete nucleotide and AA sequences are given in EP-304720, filed May 1, 1990.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SMITHKLINE BEECHAM.
                                                                                                                                                                                                                                                         Virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gordon DM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             319
                                                                                                                                                                                                                                                                         falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 89US-0447746
  /note=
89..193
                                                                                                                   /note= "Influenza virus 82..87
                                                                                                                                                                                                                                                    (A/PR/8/34/).
                       /label= artifact
/note= "see comm
                                                                                                                                                           /label= N-terminal of NS1
                                                                                                                                                                                                      Location/Qualifiers
                                                                                        /label-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          100.0%; Score 109; DB 12; 100.0%; Pred. No. 7.4e-09; tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hollingdale
                                                                                                                                                                                                                                                                                                                         circumsporozoite; CS; vaccine; malaria;
non-structural protein 1; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     327
                       comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                        nonstructural protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         319;
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AAs 19-123 of CS protein

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RESULT
AAR13178
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                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1991-179771/25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            06-DEC-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       19-JUN-1991
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Region
                                                                                                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Polypeptide comprising immunogenic determinants from P falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (BIOM-) BIOMEDICAL RES INST
Immunogenic determinant; circumsporozoite; CS; vaccine; malaria;
                             NS1_81 (NANP) 4RLfAuth.
                                                          29-AUG-1991
                                                                                       AAR13178;
                                                                                                                    AAR13178 standard; Protein; 335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 3; Page 10; 18pp; English.
                                                                                                                                                                                             293 diekkickmekcssvfnvvns 313
                                                                                                                                                                                                         1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SMITHKLINE BEECHAM
US SEC OF THE ARMY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gordon DM,
                                                                                                                                                                                                                                                                                                                            327 AA;
                                                                                                                                                                                                                                                    Conservative
                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             89US-0447746
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             203..327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "two tetrapeptide 202
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          194..201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /label= artifact
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /label=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         note="see
                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             - AAs 288-412 of CS protein
"Region II flanking region"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  immunodominant repeat region
"two tetrapeptide repeat units"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         comments"
                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                   Score 109; DB 12;
Pred. No. 7.5e-09;
Mismatches 0;
                                                                                                                    A
                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                             Length
                                                                                                                                                                                                                                                                                 327;
                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                    0;
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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozoite (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein [NSI], [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1 (NSI_81) is linked to a synthetic sequence encoding four repeat units from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region I contg. flanking region less the 18 AA signal region. This is linked to DNA encoding Region II-contg. flanking region. The Pro residue separating the Asp (at the C-terminal of the linker) from the Region II-contg. CS flanking region is an artifact of a filled-in BamHI region is an artifact of a synthetic FoklyThIII I linker. The peptide can be used in a vaccine for protection against malaria.
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                                                                                                                                                                                                                                                                                    Polypeptide comprising immunogenic determinants from P falciparum for vaccine against malaria infection in humans.
                                                                                                                                                                                                                                                                                                                                                        Gross MS,
                                                                                                                                                                                                                                                                                                                                                                           (SMIK ) SMITHKLINE BEECHAM.
(USSA) US SEC OF THE ARMY.
(BIOM-) BIOMEDICAL RES INST
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                                                                                                                                                                                                                                                          Example 4; Page 11; 18pp;
                                                                                                                                                                                                                                                                                                                            WPI; 1991-179771/25
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Sequence
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                                                                                                                                                                                                                                                                                                                                                        Gordon DM,
335 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /label= artifact
/note="see comments"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /label= AAs 19-123 of CS protein
/note= "Region 1 contg. flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /label= AAs 288-412 of CS prote= "Region II flanking
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            211..335
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /label= synthetic linker
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= N-terminal of NS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   label= artifact
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                                                                                                                                                                                                                                                          English.
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g region"
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Query Match
Best Local Similarity
Matches 21; Conserv

100.0%; Score 109; DB 12; ilarity 100.0%; Pred. No. 7.7e-09; Conservative 0; Mismatches 0;

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RESULT
AAR13179
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The polypeptide is prepd. by genetic engineering of genes encoding the P. falciparum circumsporozolte (CS) protein [Dame et al., Science 225: 593 (1984)], and the influenza virus non-structural protein 1 (NS1), [Baez et al., Nucleic Acids Research, 8: 5845 (1980)]. The DNA encoding the 1st 81 AAs of the N-terminal of NS1 (NS1_81) is linked to a synthetic sequence encoding four repeat units (the variant form) from the immunodominant region, which in turn is linked via a synthetic sequence to DNA encoding Region I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Key
Region
                                                                                                                                                WPI; 1991-179771/25
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                                                                                           Example 5; Page 11; 18pp;
                                                                                                                Polypeptide comprising immunogenic determinants from P for vaccine against malaria infection in humans.
                                                                                                                                                                     Gross
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunogenic determinant;
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US SEC OF THE ARMY.
BIOMEDICAL RES INST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            influenza virus; non-structural protein
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                                                                                                                                                                    Gordon DM,
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/note-"see
211..335
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98..103
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105..2
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"Region 1 contg. flanking
signal sequence"
                                                                                                                                                                                         TNST
                                                                                                                                                                                                                                                                                                                 * AAs 288-412 of CS protein 
"Region II flanking region"
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                                                                                                                                                                   Hollingdale MR;
                                                                                                                                                                                                                                                                                                                                                                                                                                      artifact
                                                                                                                                                                                                                                                                                                                                                                                                                                                         synthetic linker
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four variant tetrapeptide re
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            circumsporozoite; CS; vaccine; malaria; non-structural protein 1; fusion.
                                                                                           English.
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                     Chimeric - Chimeric - Chimeric -
                                                                                                                        (NAIM-)
         Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           contg. flanking region less the 18 AA signal region. This is linked to DNA encoding Region II-contg. flanking region. The Proresidue separating the Asp (at the C-terminal of the linker) from the Region I-contg. CS flanking region is an artifact of a filled-the Region I step: the Gly separating the Region I and II-contg. CS flanking regions is an artifact of a synthetic Fokk/TthIII I flanking regions is an artifact of a synthetic Fokk/TthIII I linker. The peptide can be used in a vaccine for protection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; v T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70278 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  linker. The peptide can be unagainst malaria. See also AAR12306-R12311 and
                                                                                                                                                                                                                02-MAR-2000
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                                                                                                                                                                                                                                                                                          Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                 liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-apical membrane antigen-1; AMA-1; errorste binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              06-JUN-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAY70278;
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                                                            N-PSDB;
                                                                                                   Lal AA,
                                                                                                                                                                21-AUG-1998;
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                                                           2000-237654/20.
)B; AAZ51336.
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US DEPT HEALTH & HUMAN
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Clostridium
Plasmodium f.
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                                                                                                                                                                                                                                                                                         /note= '23..350
                                                                                                                                                                                                                                                                             /label= Mature_CDC/NIIMALVAC-1
                                                                                                                                                                                                                                                                                                     /label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                   Hasnain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDC/NIIMALVAC-1.
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falciparum
                                                                                                                                                                                                                                                                 "Recombinant multivalent malarial vaccine"
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                                                                                                                            SERVICES
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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His)6 tag, T-cell epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite from tetanus toxoid and 21 antigenic epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage protein-1 (LSA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Fig27. These epitopes were obtained at different stages of the life cycle of plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial antiparamia. The color of the c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sequence encoded by the circumsporozoite (CS) gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Key
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                                                                                                                                                                                                                                                                                                                                                                                                                    30-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25-JAN-1988;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EP278940-A.
                                                                                                                                                                         WPI; 1988-229751/33.
N-PSDB; AAN81108.
                                                                  DNA encoding hepatitis used for expression in
                                                                                                                                                                                                                                                                                                                                          (SMIK ) SMITH KLINE-RIT
                                        vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                                                                                                                                   De Wilde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Region 147..206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88EP-0870008
                                                                                                                                                                                                                                                                                                                                                                                                                    87US-0009325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="Repeat region,
211..286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="Repeat region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Repeat region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            52pp; English.
                                                                                                                                                                                                                                                                                       ĭ
                                                                             B viru
yeast
                                                                                virus antigens and hybrids contg. them east to obtain vaccines and bivalent
                                                                                                                                                                                                                                                                                           Harford
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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pred. No. 8.1e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              probe; hybridisation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                              z
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat unit = NANP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      repeat unit =
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        repeat unit =
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        from
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Sequence

412 AA

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SXCCCCCCXXX
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AAP60416
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence of the CS gene (AANB1108) is from lambda-mpfl. A recombinant DNA molecule is claimed, comprising functional DNA coding sequence fused, in phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) in phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) in phase, to a portion of the Pre-S2 region of a hepatitis B virus (HBV) comprises the Pre-S2 coding sequence. The functional DNA coding sequence comprises the Pre-S2 coding sequence, the CS protein coding sequence of Pre-S1-Pre-S2 coding sequence, the CS protein coding sequence of Plasmodium, or a HIV coding sequence such as an HIV envelope gene sequence, e.g. HIV C7 protein coding region, HIV peptide 121 coding region, or HIV Dreesman peptide coding region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example; Fig 3Aa-3Af; 101pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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                                                                                                                                                                                                                                                                                                                                                                                          Key
Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sporozoite;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CS protein
                                                                                                                                                                                                                          (USDC ) US
(USGO ) US
(USSA ) US
                                                                                                                                                                                                                                                                                                                             02-JAN-1986
                                                                                                                                                                                                                                                                                                                                                       EP166410-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        377 diekkickmekcssvfnvvns
                                                                                                                                                             WPI; 1986-008635/02.
N-PSDB; AAN60362.
                                                                                                                                                                                                                                                                              26-JUN-1984;
                                                                                                                                                                                                                                                                                                     24-JUN-1985;
                     The plasmodium CS gene was used to isolate peptides capable of inducing an immune response to the parasite. Peptide antigens be synthesised in pure form and used to generate an immune response in vaccination against malaria. The featured repeat units are claimed and must be present in copies of 2-1000.
                                                                                                                        New immunologically active pure synthetic peptide(s) - protection against infection by malaria parasite.
                                                                                                 Disclosure; Fig 2; 49pp;
                                                                                                                                                                                                   McCutchan TF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 DIEKKICKMEKCSSVENVVNS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        411 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of malaria parasite
                                                                                                                                                                                                                                                                                                                                                                                                                                   falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                              GOVERNMENT.
SEC OF THE ARMY.
                                                                                                                                                                                                                                                       SEC OF COMMERCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         vaccination
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                                                                                                                                                                                                                                                                               84US-0624564
                                                                                                                                                                                                                                                                                                        85EP-0107794
                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
124..127
                                                                                                                                                                                                                                                                                                                                                                                  /label= Repeat unit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 412
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%;
                                                                                                                                                                                                       JВ,
                                                                                                     English.
                                                                                                                                                                                                        Williams
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            397
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 109; DB 9;
NO. 9.6e-09;
0;
                                                                                                                                                                                                          JL,
                                                                                                                                                                                                             Schneider
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 411;
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
the cloning procedure used to construct the hybrid gene, a stretch of 189 amino acids representing amino acids 210 to 398 of the circumsporozoite protien (CSP) of Plasmodium falciparum strain 768, an amino acid Arg created by the cloning procedure, four amino acids, pro-Val-Thr-Asn, representing the four carboxy terminal residues of hepatitis B virus (HBV), adw serotype, pre52 protein, and a stretch of 226 amino acids specifying the S protein of HBV, adw serotype.
                                                                           This sequence represents the RTS hybrid protein which is encoded by the RTS expression cassette. This hybrid consistits of a methionine residue derived from S. cerevisiae TDH3 gene sequence, three amino acids, Met-Ala-Pro, derived from a nucleotide sequence created by
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RTS
                                                                                                                                                                 Hybrid protein comprising Plasmodium circumsporozoite protein and {\sf HBSAg} - useful as a vaccine for treating patients susceptible to
                                                                                                                                                                                                                                                                              16-NOV-1991;
27-FEB-1992;
                                                                                                                                                                                                                                                                                                              11-NOV-1992;
                                                                                                                                                                                                                                                                                                                                    27-MAY-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cloning; ci
strain 7G8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAR37796
                                                                                                                                   Disclosure;
                                                                                                                                                                                                    N-PSDB;
                                                                                                                                                                                                                                    Cohen
                                                                                                                                                                                                                                                                                                                                                          W09310152-A.
                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                          Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Region
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                                                                                                                                                                                                                                                         (SMIK)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIEKKICKMEKCSSVFNVVNS 21
                                                                                                                                                                                                   1993-182494/22.
DB; AAQ42566.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    diekkickmekcssvfnvvns 398
                                                                                                                                                                                                                                   ŗ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                         SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ression cassette; hybrid protein; S. cerevisiae; TDH3; circumsporozoite protien; CSP; Plasmodium falciparum; G8; hepatitis B virus; HBV; adw serotype; preS2 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               standard;
                                                                                                                                                                                                                                   De
                                                                                                                                                         infections
                                                                                                                                  Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                    Wilde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first
                                                                                                                                                                                                                                                                             91GB-0024390.
92US-0842694.
                                                                                                                                                                                                                                                                                                              92WO-EP02591
                                                                                                                                   5.
                                                                                                                                                                                                                                                                                                                                                                                           198..424
                                                                                                                                                                                                                                                                                                                                                                               /note-
                                                                                                                                                                                                                                                                                                                                                                                                              /note=
                                                                                                                                                                                                                                                                                                                                                                                                                          194..197
                                                                                                                                                                                                                                                                                                                                                                                                                                               /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
                                                                                                                                   59pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Cloning artefact"
                                                                                                                                                                                                                                                                                                                                                                                                                                              "Represents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *Derived from S. cerevisiae
                                                                                                                                                                                                                                                                                                                                                                                                   "Carboxy terminal serotype) preS2 p
                                                                                                                                                                                                                                                                                                                                                                              "S protein of HBV
                                                                                                                                   English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 109; DB 7;
Pred. No. 9.6e-09;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                               amino
                                                                                                                                                                                                                                                                                                                                                                                           2 protein"
                                                                                                                                                                                                                                                                                                                                                                             (adw serotype)"
                                                                                                                                                                                                                                                                                                                                                                                                                                              acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0
                                                                                                                                                                                                                                                                                                                                                                                                                                               210-398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TDH3
                                                                                                                                                                                                                                                                                                                                                                                                               from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         gene
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                                                                                                                                                                                                                                                                                                                                                                                                             (adw
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RESULT 12
AAR37797
SXCCCC
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Best Local S
Matches 21
                                                                                                                                                                                                                                                                                                                                                                                                                        RTS*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This protein, and RTS* (see also AAR37797), may be combined with an adjuvant and used in a vaccine for preventing plasmodium infections. The vaccines produce a humoral response and also a cellular immune.
                                                                                                                Cohen J,
                                                                                                                                                                                                                                                                                                                                                                                    RTS; expression cassette; hybrid protein; S. cerevisiae; TDH3; cloning; circumsporozoite protien; CSP; Plasmodium falciparum; strain 7G8; hepatitis B virus; HBV; adw serotype; preS2 protei
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR37797 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                           Hybrid protein comprising Plasmodium circumsporozoite HBsAg - useful as a vaccine for treating patients susc
                                                                                                                                                  16-NOV-1991;
27-FEB-1992;
                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                          Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                        27-SEP-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR37797;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     response
                                                                                       N-PSDB;
                                                                                                                                                                             11-NOV-1992;
                                                                                                                                                                                              27-MAY-1993
                                                                                                                                                                                                               WO9310152-A
                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                              Protein
                                                                                                                                                                                                                                                                                                              Region
                                                                                                                                                                                                                                                                                                                                 Region
                                                    Plasmodium
                                                                                                                                 (SMIK ) SMITHKLINE BEECHAM BIOLOGICALS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      173 diekkickmekcssvfnvvns
                                                                                                                                                                                                                                                                                                                                                                           protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity 100 hes 21; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 DIEKKICKMEKCSSVFNVVNS
                                                                                               1993-182494/22
                                                                                     AAQ42567
                                                                                                                De Wilde M;
                                                    infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     424 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                   91GB-0024390
92US-0842694
                                                                                                                                                                             92WO-EP02591
                                                                                                                                                                                                                                          198..424
                                                                                                                                                                                                                                /note-
                                                                                                                                                                                                                                                          /note-
                                                                                                                                                                                                                                                                    194..197
                                                                                                                                                                                                                                                                                     /note= "Represents amino
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                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Protein; 424
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                                                                                                                                                                                                                                                "Carboxy terminal amino serotype) preS2 protein
                                                                                                                                                                                                                                                                                                      "Cloning artefact"
                                                                                                                                                                                                                                                                                                                        "Derived
                                                                                                                                                                                                                                "S protein of HBV (adw serotype)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       193
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21
                                                                                                                                                                                                                                                                            falciparum"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 109; DB 14;
Pred. No. 9.9e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                        from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ₹
                                                                                                                                                                                                                                                                                                                        s
                                                                                                                                                                                                                                           protein"
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                                                           susceptible
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                                                                                                                                                                                                                                                                                                                       sequence*
                                                             and
to
                                                                                                                                                                                                                                                                                     CSP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                     of.
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This sequence represents the RTS* hybrid protein which is encoded by the RTS* expression cassette. This hybrid consisits of a methionine residue derived from S. cerevisiae TDH3 gene sequence, three amino

Disclosure;

Fig 9;

59pp;

English.

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RESULT 13
AAABOOR TARESTORY
AAABOOR TARABOOR TAR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   acids, Met-Ala-Pro, derived from a nucleotide sequence created by the cloning procedure used to construct the hybrid gene, a stretch of 189 amino acids representing amino acids 210 to 389 of the circumsporozoite protien (CSP) of Plasmodium falciparum strain NF54, an amino acid Arg created by the cloning procedure, four amino acids, pro-Val-Thr-Asn, representing the four carboxy terminal residues of hepatitis B virus (HBV), adv serotype, pre52 protein, and a stretch of 256 amino acids specifying the S protein of HBV, adv serotype. This protein, and RTS (see also ARR37796), may be combined with an adjuvant and used in a vaccine for preventing plasmodium infections. The vaccines produce a humoral response and also a cellular immune
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Circumsporozoite gene; Plasmodium falciparum; lambda mPf1; vaccine; yeast glyceraldehyde-3P-dehydrogenase gene (TDH3) promoter; yeast ornithine carbamoyl transferase gene (ARG3); repeat region.
Plasmid WR201 was obtained Research, and results from
                                                                                               Example 1; Fig 2a; 44pp; English.
                                                                                                                                                                     expression
                                                                                                                                                                                   Expression of P. falciparum circumsporozoite protein by yeast using recombinant DNA vector having coding sequence linked to
                                                                                                                                                                                                                                                                                                                                                                                                    De Wilde
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-1987;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     11-SEP-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence encoded by the circumsporozoite (CS) gene of Plasmodium falciparum in lambda mpfl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAP80835;
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DB; AAN81781.
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148..207
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers 124..147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="repeat region,
                                                                                                                                                                     sequence
from the Walter Reed Army Institute of insertion of a 2.3 kb EcoRI fragment f
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ΑA
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RESULT 14
AAP91594
ID AAP915
AC AAP915
XX Sequen
XX Circum
KW Circum
KW Vaccin
OS Plasmo
FFI Misc-d
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Best Local
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   Peptide CS.T3 (residues 1-21) corresponds to residues 378-398 of the CS protein from P. falciparum but contains 2 Ala residues in place
                                                                                             Claim 1; Page 16; 23pp; English
                                                                                                                                                                                          Modified Plasmodium CS peptide - used as a universally recognised T-cell epitope in vaccines to elicit an immune response against
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers Misc-difference 1..2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         13-MAR-1992 (first entry)
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                                                                                                                                                             pathogenic
                                                                                                                                                                                                                                                                                                                                                       Sinigaglia F;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-MAY-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                    (HOFF ) HOFFMANN-LA ROCHE AG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified Plasmodium circumsporozoite T-cell epitope CS.T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        88GB-0012214.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     89EP-0108618
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19..21
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95.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    21
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Pred. No. 3.9e-08;
1; Mismatches 0
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Best Local :
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Best Local Similarity
Matches 19; Conserv
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                                                                                          AAR82571-91 are helper T cell epitopes which can be used in the preparation of a peptide immunogen that is useful in vaccines for treating allergic reactions. In the immunogen an IgE CH4 peptide is attached C-terminally to a series of amino acids including a helper T cell epitope. The immunogen may also opt. contain a fatty acid or fatty acid derivative, an invasin domain or alpha-NH2. The immunogen produces high titres of antibodies to the effector site in human IgE heavy chain (the CH4 domain peptide) which inhibit mast cell activation and reduce allergen-induced IgE prodn. The immunogens may be used in either a radially branching multimeric form or a linearly arranged monomeric form.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the native protein's Cys residues at positions 384 and 389. Also claimed is AAP91504 (or modified forms, see FT) associated with an antigenic structure representing a B-cell epitope, pref. a multiple antigenic peptide, esp. multimers of the repeat sequences NANP present in P. falciparum CS protein.
                                                                                                                                                                                                                                                                         Claim 3; Page 23; 87pp; English.
                                                                                                                                                                                                                                                                                                                 Synthetic peptide-based immunogen contg. IgE CH4 peptide and helper T cell epitope - useful for eliciting antibody prodn. for allergy
                                                                                                                                                                                                                                                                                                                                                                 WPI; 1995-351297/45
                                                                                                                                                                                                                                                                                                                                                                                             Wang CY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-OCT-1994;
28-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             05-OCT-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IgE; CH4; immunoglobulin; epsilon; immunogen; helper T cell; epitope;
vaccine; allergy; antibody; constant heavy chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-JUN-1996 (first entry)
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                                                                      Sequence
                                                                                                                                                                                                                                                                                                        treatment
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                                                                                                                                                                                                                                                                                                                                                                                                                      (UNBI-) UNITED BIOMEDICAL INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                24-MAR-1995;
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les 19; Conserv
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   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                        AA;
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94US-0218461.
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               83.5%;
90.5%;
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Pred. No. 2.4e-07;
Pred. No. 2;
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Score 91; DB 16;
Pred. No. 2.4e-07;
0; Mismatches 2;
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                           Length 21;
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Search completed: January 29, 2002, 10:21:43 Job time: 419 sec

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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                    Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score
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1: /cgn2_6/ptodata/2,
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US-08-760-797A-1
US-08-760-797A-3
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US-08-932-929B-3
US-08-186-266-6
US-08-446-992-4
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	1 DIEKKICKMEKOSSVFNVVNS 21	Match 100.0%; Score 109; DB 1; Length 412; Local Similarity 100.0%; Pred. No. 8.4e-09; es 21; Conservative 0; Mismatches 0; Indels 0;	TELEPHONE: (212) 278-0400 TELEFAX: (212) 391-0526 INFORMATION FOR SEQ ID NO: 18: SEQUENCE CHARACTERISTICS: SEQUENCE CHARACTERISTICS: LENGTH: 412 amino acids TYPE: amino acid TYPE: amino acid STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: peptide -08-313-288B-18	MM: WM: y disk y disk compatible PC-DOS/MS-DOS Release #1.0, Version #1. ATA: US/08/313,288B US/08/313,288B rry 5, 1995 187ION: P. BATION: P. CORMATION:	EXOUENCES: 20 NCE ADDRESS: : Cooper & Dunham LLP 1185 Avenue of the Americas w York ew York USA 36	ESULT 1 5-08-313-288B-18 Sequence 18, Application US/08313288B Patent No. 5750502 GENERAL INFORMATION: APPLICANT: Jessell, Thomas M. and Avihu Klar TITLE OF INVENTION: CLONING, EXPRESSION AND US TITLE OF INVENTION: NOVEL SECRETED PROTEIN, F-	3 39 35.8 77 2 US-08-634-641-58 Sequence 58, 4 39 35.8 77 2 US-08-634-641-58 Sequence 58, 5 39 35.8 77 3 US-09-249-471-58 Sequence 58, 6 39 35.8 77 3 US-09-	9 48 44.0 15 2 US-08-318-856A-76 Sequence 76, 0 47 43.1 492 4 US-08-845-258-21 Sequence 21, 1 47 43.1 492 4 US-08-90-571-21 Sequence 21, 2 47 43.1 503 4 US-08-90-571-52 Sequence 21, 3 47 43.1 503 4 US-08-90-571-52 Sequence 52, 4 47 43.1 503 4 US-08-90-571-52 Sequence 52, 4 47 43.1 503 4 US-08-90-571-72 Sequence 52, 4 47 43.1 503 4 US-08-90-571-72 Sequence 7, p. 6 46 42.2 1400 3 US-08-465-713-7 Sequence 7, p. 7 46 42.2 1400 3 US-08-165-77 Sequence 7, p. 8 46 42.2 1400 5 PCT-US93-05857-7 Sequence 7, p. 9 39.5 36.2 159 6 5208144-35 9 39.5 8 77 2 US-08-465-380-58 Sequence 58, p. 1 39 35.8 77 2 US-08-465-380-58 Sequence 58, p. 2 35.8 77 2 US-08-465-390-58 Sequence 58, p. 3 35.8 77 2 US-08-486-397-58 Sequence 58, p. 3 36.8 77 2 US-08-486-397-58 Sequence 58, p. 3 37 38 38 78 79 79 18 78 78 78 78 78 78 78 78 78 78 78 78 78	0 55 5 0 16 5 000-0500-05016 000-050 16 00

RESULT 2 US-08-760-797A-1

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                                                                                                                                                                                                                                                            US-08-760-797A-3
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APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: from Plasmodium and HBSAG
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 109; DB 2; Best Local Similarity 100.0%; Pred. No. 8.6e-09; Matches 21; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                       GENERAL INFORMATION:
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OPERATING SYSTEM: DOS
SOFTWARE: PastSEO for Windows Version 2.0
CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 33,833
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE CHARACTERISTICS:
LENGTH: 423 amino acids
                                                                                                    APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: SmithKilne beech symplet: 709 Swedeland Road CITY: King of Prussia
                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: SmithKline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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CLASSIFICATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 423 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: 610-270-5090
              STREET: 709 Swedeland CITY: King of Prussia STATE: PA
COUNTRY:
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5. 5928902
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TOPOLOGY: US-08-760-797A-3
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Patent No. 6169171
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Best Local (
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FILING DATE: 04-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/442,612
APPLICATION NUMBER: 08/442,612
APPLICATION NUMBER: 08/442,612
APPLICATION NUMBER: 08/442,612
APPLICATION TOWNSTION:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
TITLE OF INVENTION: Hybrid Protein Between CS
TITLE OF INVENTION: from Plasmodium and HBsAG
                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                   ZIP: 19406
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: SmithKline Beecham Corporation
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APPLICATION NUMBER: 08/760,797
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
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                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH:
                                                                                                                                                                                                                                                                                                                   STREET: 709 Swedeland CITY: King of Prussia STATE: PA
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OPERATING SYSTEM:
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ZIP: 19406
                                                                                                                                                              APPLICATION NUMBER: US/08/932,929B
NAME: Baumeister, K
REGISTRATION NUMBER:
                                                                                                                                     CLASSIFICATION:
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Similarity 100.0%;
21; Conservative 0
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   Kirk
2R: 33,833
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Pred. No. 8.7e-09;
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                                                            US-08-932-929B-3
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Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Applic Patent No. 6169171
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 424 amino acid
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                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 424 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                       FILING DATE: 17-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Baumeister, Kirk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Smithkline Beecham Corporation
STREET: 709 Swedeland Road
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REPERENCE/DOCKET NUMBER: B45015-1FWC2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                             TELECOMMUNICATION INFORMATION: TELEPHONE: 610-270-5096
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: De Wilde, Michel
APPLICANT: Cohen, Joseph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/760,797
FILING DATE: 04-DEC-1996
APPLICATION NUMBER: 08/442,612
FILING DATE: 17-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STREET: 709 SWELLER CITY: King of Prussia
                                                                           TOPOLOGY: 11
                                                                                                       TYPE:
                                                                                                                                                                                                                                       NAME: Baumeister, Kirk REGISTRATION NUMBER: 3
                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                  TELEX:
                                                                                                                                                                              TELEFAX:
                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: B45015-1FWC2
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                     amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Application US/08932929B
                                                                                                                424 amino acids
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                                                                                                                                                                                610-270-5090
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ilarity 100.0%;
Conservative 0
                                                                          linear
                                                                                      single
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hybrid Protein Between CS from Plasmodium and HBsAG
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                                                                                                                                                                                                                                   33,833
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Pred. No. 8.7e-09
Score 109; DB 4; Pred. No. 8.7e-09;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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             Length 424;
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; OTHER INFORMATION: ; OTHER INFORMATION: US-08-186-266-6
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ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: PLOPPY DISK
MEDIUM TYPE: PLOPPY
Query Match
Best Local Similarity
Matches 19; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 01
FILING DATE: 29-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 01
FILING DATE: 06-AUG-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: Patentin Rel CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 07-AUG-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PILING DATE: 06-AUG-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/027,746

FILING DATE: 05-WAR-1993

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/926,666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION: 424
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: INDUCTION OF ANTI-TUMOR CYTOTOXIC TITLE OF INVENTION: TLYMPHOCYTES IN HUMANS USING TITLE OF INVENTION: SYNTHETIC PEPTIDE EPITOPES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT:
                                                                                                                                                                                                                                                                                                                                              FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                      MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: FILING DATE: 25-JA
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                                                                                                                                                                                                                                                                 NAME/KEY: Peptide LOCATION: 1..21
                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 34,774
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                                                                                                                                                                                                                                                                                                                                                                                                                                        amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bastian, Kevin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Application US/08186266
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SETTE, Alessandro
CELIS, Esteban
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GREY,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                         linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (415) 543-9600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-JAN-1994
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                                  90.5%;
                                                                                                                                                                                                  /note= "Plasmodium falciparum
protein at positions 378-398."
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                               Score 91; DB 1;
Pred. No. 2.1e-07;
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                                                              Length 21;
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Conservative

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                                                                                                                                                                                                                           Sequence 48, Patent No. 5
                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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Best Local
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APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
ADDRESSE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY ACENT INFORMATION:
NAME: MATIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEPAX: (516)751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                        TITLE OF INVENTION: immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
                                                                                                                                                   APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
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ZIP: 10154-0053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: US/08/446,692 FILING DATE: 7-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: amino acid TOPOLOGY: linear
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                STREET:
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                                                                                                                                                                                                                                                                                                                                        1 DIEKKICKMEKCSSVFNVVNS 21
|||||| ||| |||||||||
1 DIEKKIAKMEKASSVFNVVNS 21
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                                                                                                                                                                               9, Application US/08488351A 5843446
New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                       83.5%; Score 91; DB 1; 90.5%; Pred. No. 2.1e-07;
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RESULT 9
US-09-100-409A-54
; Sequence 54, Application US/09100409A
; sequence 56090388

satent No. 6090388
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ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION MUMBER: US/08/488,351A
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 19; Conserv
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PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/446,692
FILLING DATE: 7-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US 08/229,275
APPLICATION UNMBER: US 08/229,275
FILING DATE: 14-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (516)/51-0049
INFORMATION FOR SEQ ID NO: 48:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION: 424
ATTORNEY_AGENT INFORMATION:
NAME: MATIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE_/DOCKET NUMBER: 1151
TELEPHONE: (212)415-8745
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
              ZIP: 10154-0054

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, V

SOFTWARE: #1.25

CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION UMBER: US 08/057,166
FILING DATE: 27-APR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: 11
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH:
                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                           CITY: New York
STATE: NY
                                                                                                                                                                                                                  ADDRESSEE: MOKUM. Avenue
                                                                                                                                                        COUNTRY: USA
ZIP: 10154-0054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIEKKIAKMEKASSVFNVVNS 21
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APPLICATION NUMBER: US/09/100,409#
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                                                                                                                                                                                                                                                                                                                                                                          Wang, Chang Yi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                           USA
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                                                                                                                                                                                                                                                                                                                                   PREVENTION AND TREATMENT OF HIV INFECTION AND
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                                                                                                                                                                                                                                                                                                             IMMUNE DISORDERS
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Pred. No.
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PCT-US95-02121-97
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Best Local 9
                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US 08/
FILING DATE: 16-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/
FILING DATE: 26-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                    TELEFAX: (415) 543-5043 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 07/874,491
FILING DATE: 27-APR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,682
FILING DATE: 29-JAN-1992
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
                                                                                                      REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-26-4PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: 1
FILING DATE: 26-AUG-
                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide
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Local Similarity 90.5%;
nes 19; Conservativo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: PCT/US95/02121 FILING DATE: 16-FEB-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: CLASSIFICATION:
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STRANDEDNESS:
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1 DIEKKIAKMEKASSVFNVVNS 21
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                                 ENGTH:
              amino acid
                                                                                                                                                                          Parmelee, Steven W
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                             21 amino acids
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SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                 JMBER: US 07/749,568
26-AUG-1991
unknown
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Pred. No. 2.1e-07;
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Gaps

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PCT-US95-13841-20
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                                                          Matches
                                                                       Query Match
Best Local
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US9
FILING DATE: 25-OCT-1995
                                                                                                                                                                                                                     TELEX: 421792
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: United Biomedical Inc; Walfield, Alan M.;
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IgE Membrane Anchor
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
NUMBER OF SEQUENCES: 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 212-758-4800 TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/328,519
FILING DATE: 25-OCT-1994
                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION: NAME: Lin, Maria C.H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LOCATION: 1..21
OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                          NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: New York
STATE: NY
                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
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                             1 DIEKKICKMEKCSSVENVVNS 21
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                                                                       Similarity
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345 Park Avenue
                                                                                                                                                                                        21 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  USA
                                                        Conservative
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                                                                       83.5%;
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378-398"
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Pred.
                                                          0;
                                                                       Score 91;
Pred. No.
                                                          Mismatches
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                                                      2.1e-07;
2;
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2.1e-07;
                                                                                   Length 21;
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US-08-446-692-27; Sequence 27, Ap; Patent No. 5759
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                                                                                                                                                                                                                                                                                                                      Sequence 27, Application Patent No. 5843446
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
NAME: MATIA C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 27:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 1
                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                APPLICANT: Ladd, Anna APPLICANT: Wang, Chang Yi APPLICANT: Zamb, Timothy
                                                                                                                                                                                                        TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: US/
FILING DATE: 7-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                COUNTRY:
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                                                                                                                New York
                                                                                                                                                                                                                                                                                                                                            7, Application US/08488351A 5843446
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)GY: linear
                                                                              10154-0053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    83.5%; Score 91; I
90.5%; Pred. No. 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/446,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1151-4146 US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 33;
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; TOPOLOGY: linear; MOLECULE TYPE: peptide US-08-488-351A-27
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Patent No.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Hoffma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEPAX: (516)751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
CLASSIFICATION: 424
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PRIOR APPLICATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PatentIn Release #1.0, Version CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/488,351A
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Hoffman, Stephen L. APPLICANT: Hedstrom, Richard C. APPLICANT: Sedegah. Marth-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
                                                                              SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/155,888
                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
                            CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                        STREET: Bldg. 1, T-12 8901 Wisconsin Ave. CITY: Bethesda STATE: Marvland
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: FILING DATE: 14-API
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 7-JUN-1995
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                                                                                                                                                                                                                ZIP:
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NAME: Spevack, A. David REGISTRATION NUMBER: 24
                                                                                                                                                                                                                           COUNTRY:
                                                                     FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                     POLYNUCLEOTIDE VACCINE PROTECTIVE AGAINST MALARIA, METHODS OF PROTECTION AND VECTOR FOR DELIVERING POLYNUCLEOTIDE VACCINES
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90.5%; Pred. No.
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/08/465,167A
FILING DATE: 05-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 08/103,623
FILING DATE: 06-AUG-1993
ATTORNEY/AGENT INFORMATION:
NAME: Patmelee, Steven W.
REGISTRATION NUMBER: 31,990
REFERENCE/DOCKET NUMBER: 14137-60-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 206-467-9600
TELEPHONE: 206-467-9600
INFORMATION TOR SED ID NO: 20:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 δõ
                                                                                                  ; TOPOLOGY: linear; MOLECULE TYPE: protein US-08-465-167A-20
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US-08-465-167A-20
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; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-155-888-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 20, Application US/08465167A
Patent No. 5750395
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Fikes, John D.
APPLICANT: Livingston, Brian D.
APPLICANT: Sette, Alessandro D.
APPLICANT: Sidney, John C.
TITLE OF INVENTION: DNA ENCODING MAGE-1 C-TERMINAL
TITLE OF INVENTION: IMMUNOGENIC PEPTIDES (as amende
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 76.1%;
Best Local Similarity 61.9%;
Matches 13; Conservative
Best Local Similarity 85.7 Matches 18; Conservative
                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (202) 295-1022 INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 478 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DIEKKICKMERCSSVFNVVNS 21
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444 DIDTEICKMDKCSSIFNIVSN 464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 98111
                                                                                                                                                        LENGTH: 20 amino acids
TYPE: amino acid
STRANDEDNESS: single
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CITY: San Francisco
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                  69.3%;
85.7%;
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Score 75.5; DB 1;
Pred. No. 3.9e-05;
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 83; DB 3;
Pred. No. 6.6e-05;
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Search completed: January 29, 2002, 10:24:03 Job time: 509 sec

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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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Perfect score:
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pir3:*
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GenCore version 4.5 (c) 1993 - 2000 Comp
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A29319
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OZZQAV
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D41156
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A54504
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0ZZQAB
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OZZQAF
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11.035 Million cell updates/sec
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                           circumsporozoite
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ALIGNMENTS

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circumsporozoite protein - malaria parasite (Plasmodium falciparum) (isolate IMTM22) c;Species: Plasmodium falciparum C;Species: Plasmodium falciparum C;Date: 15-Nov-1984 #sequence_revision 15-Nov-1984 #text_change 09-Jun-2000 C;Accession: A03388 R;Dame, J.B.; Williams, J.L.; McCutchan, T.F.; Weber, J.L.; Wirtz, R.A.; Hochmeyer, W
                                                                                                                                         RESULT
OZZQAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: EMBL:x15363
R;Caspers, P.; Gentz, R.; Matile, H.; Pink, J.R.; Sinigaglia, F.
MOI. Biochem. Parasitol. 35, 185-190, 1989
A;Title: The circumsporozoite protein gene from NF54, a Plasmodium falciparum isolate A;Reference number: A45527; MUID:89364998
A;Accession: A45527
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A;Residues: 319-336,354-373 <LOC>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;329-383/Domain: thrombospondin type 1 repeat homology <THR1>
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A;Molecule type: DNA
A;Residues: 1-405 <CAS>
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A; Residues: 1-405 < CAM>
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A; Title: DNA sequence of the gene encoding
A; Reference number: S05428; MUID:89345189
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C;Date: 07-Jun-1990 #sequence_revision
C;Accession: S05428; A45527; I60657
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Pred. No. 1.5e-08;
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A;Molecule type: DNA
A;Residues: 1-412 <DAN>
A;Residues: GB:K02194; NID:g160160; PIDN:AAA29524.1; PID:g160161
A;Cross-references: GB:K02194; NID:g160160; PIDN:AAA29524.1; PID:g160161
A;Experimental source: clone 7G8
C;Comment: Residues 1-16 are the probable signal sequence.
C;Comment: There are 41 copies of a 4-residue repeating unit in the midd C;Comment: There are 41 copies of a 4-residue repeating unit in the midd C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat how F;336-390/Domain: thrombospondin type 1 repeat homology <THR1>
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Rod. Biochem, Parasitol. 24, 289-294, 1987

A); Title: Circumsporozoite gene of a Plassmodium falciparum strain from Thailand.

A, Reference number: A54533; MUID:87315205

A; Accession: A54533

A; Status: preliminary

A; Kolecule type: DNA

A; Rolecule type: DNA

A; Rolecule type: DNA

A; Residues: 1-424 <DEL>

A; Cross-references: GB:H09752; NID:g160216; PIDN:AAA29555.1; PID:g160217

C; Superfamily: circumsporozoite protein: thrombospondin type 1 repeat homology

F; 348-402/Domain: thrombospondin type 1 repeat homology
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A;Title: Structure of the gene encoding the A;Reference number: A03388; MUID:84250215
A;Accession: A03388
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A;Accession: A54529
A;Accession: A54529
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary; not compared with conceptual translation
A;Status: preliminary
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecules: 1-442 <CLOC>
A;Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1; PID:g160215
A;Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1; PID:g160215
A;Cross-references: GB:M15505; NID:g160214; PIDN:AAA29554.1; PID:g160215
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C; Accession: A54529

A54529

CESPECIA: A RESULT

ASAGRAPH 
                                                                                                                                                              c;Superfamily: circumsporozoite protein; thrombospondin C;Keywords: tandem repeat F;366-420/Domain: thrombospondin type 1 repeat homology
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Pred. No. 1.5e-08;
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Pred. No. 1.5e-08;
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                                                                                                                                          N;Alternate names: sporozoite surface a C;Species: Plasmodium berghei C;Date: 30-Sep-1987 #sequence_revision C;Accession: A44948; A25083; S13446
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circumsporozoite protein - Plasmodium reichenowi
C;Species: Plasmodium reichenowi
C;Date: 14-Feb-1992 *sequence_revision 14-Feb-1992
C;Accession: A39756
R;Lal, A.A.; Goldman, I.F.
J. Biol. Chem. 266, 6686-6689, 1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT
A39756
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A;Residues: 1-388 <LAL>
A;Residues: 1-388 <LAL>
A;Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229
A;Cross-references: GB:M60972; NID:g160228; PIDN:AAA29561.1; PID:g160229
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
F;312-366/Domain: thrombospondin type 1 repeat homology <THR1>
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A;Accession: A39756
A;Status: preliminary
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                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-264 <COL>
A; Cross-references: GB: M32350
A; Cross-references: GB: M32350
C; Superfamily: Circumsporozoite protein; thrombospondin
F; 190-242/Domain: thrombospondin type 1 repeat homology
                                                                                                                                                                                                                                                                                                                                                                                       circumsporozoite protein precursor - Plasmodium yoelii nigeriensis
C;Species: Plasmodium yoelii nigeriensis
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 01-Dec-1995
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Pred. No.
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                                                                                                                                               6.5e-05
                                                                                                                                                              DB 2;
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.8e-08;
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circumsporozoite protein precursor - Plasmodium N;Alternate names: sporozoite surface antigen

A; Title: R;Lanar,

Sequence

٥f the

circumsporozoite

gene

of Plasmodium

berghei ANKA clone

and z

Biochem. Parasitol.

39,

151-154,

1990

28-Jul-1995

#text_change 16-Jul-1999

berghei

(strain NK65)

D.E.

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A: Molecule type: DNA
A: Residues: 1-26, 'I', 28-68, 'PMLRR', 75-126, 'P', 128-134, 'PPPNANDP', 135-332 <EIC>
A: Cross-references: GB:M14135; NID:g160245; PIDN:AAA29577.1; PID:g160246
R; Weber, J.L.; Egan, J.E.; Lyon, J.A.; Wirtz, R.A.; Charoenvit, Y.; Maloy, W.L.; Ho
Exp. Parasitol. 63, 295-300, 1987
A: Title: Plasmodium berghei: cloning of the circumsporozoite protein gene.
A: Reference number: S13446
A: Status: preliminary
A: Accession: S13446
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 61-122, 'A', 124-332 <WEB>
A: Cross-references: GB:M25445; NID:g160177; PIDN:AAA29531.1; PID:g160178
C: Comment: There are three distinct regions in the mature circumsporozoite protein.
Oblo membrane-anchoring sequence.
C: Superfamily: circumsporozoite; surface antigen; tandem repeat
F:1-23/Domain: Signal sequence #status predicted <SIG>
F:24-332/Product: circumsporozoite protein #status predicted <MAT>
F:94-189/Region: 8-residue repeats
F:94-189/Region: 8-residue repeats
A;Cross-references: EMBL:X17606

R;Lockyer, M.J.

submitted to the EMBL Data Library, November 1989

A;Reference number: S12571

A;Reference number: S12571

A;Accession: S12571

A;Rosidues: 1-59, I',61-81,83-348 <LOC2>
A;Residues: 1-59, I',61-81,83-348 <LOC2>
A;Residues: 1-59, I',61-81,83-348 <LOC2>
C;Superfamily: circumsporozoite protein; thrombospondin type 1 r.
C;Keywords: tandem repeat
F;1-20/Domain: signal sequence #status predicted <SIG>
F;21-348/Product: circumsporozoite protein #status predicted <MAP: F;21-347/Region: 8-residue repeats
F;215-247/Region: 2-residue repeats
F;215-247/Region: 1-residue repeats
F;214-326/Domain: thrombospondin type 1 repeat homology <THR1>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: sporozoite surface antigen C;SpecLes: Plasmodium berghei C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 16-Jul-1999 C;Accession: S07873; S12571 R;Lockyer, M.J.; Davies, C.S.; Suhrbier, A.; Sinden, R.E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R;Eichinger, D.J.; Arnot, D.E.; Tam, J.P.; Nusse Mol. Cell. Biol. 6, 3965-3972, 1986
A;Title: Circumsporozoite protein of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A44948; M
A;Accession: A44948
A;Molecule type; DNA
A;Residues: 1-332 <LAN>
A;Cross-references: GB:M28887
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-348 <LOC>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Title: Nucleotide sequence of the Plasmodium berghei circumsporozoite protein gene fro A; Reference number: S07873; MUID:90221834
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13; Conser
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   thrombospondin type 1 repeat homology <THR1:
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Pred. No.
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1 repeat
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J. Biol. Chem. 262, 2937-2940, 1987
A;Title: Structure of the gene encoding the
A;Reference number: A26271; MUID:87137555
A;Accession: A26271
A;Molecule
                                                                                                                                                                                                                                                                                                               Mol. Biochem. Parasitol. 30, 291-294, 1988
A;Title: Structure of the circumsporozoite gene of Plasmodium malariae.
A;Reference number: A54504; MUID:89040027
A;Accession: A54504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT
A54504
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        oblic membrane-anchoring sequence.

C;Comment: There are 15 copies of a 6-residue repeat and 8 copies of a 4-residue C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology C;Keywords: sporozoite; surface antigen; tandem repeat C;Keywords: sporozoite; surface antigen; tandem repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              circumsporozoite protein precursor - Plasmodium yoelii
N;Alternate names: sporozoite surface antigen
C;Species: Plasmodium yoelii
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F;20-367/Product: circumsporozoite protein #status predicted
F;139-228/Region: 6-residue repeats (Q-G-P-G-A-P)
F;229-260/Region: 4-residue repeats (Q-Q-P-P)
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Best Local Similarity
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                                                                                                                                                                                                      C; Superfamily: circumsporozoite protein; thrombospondin C; Keywords: tandem repeat
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A; Residues: 1-429 <LAL>
A; Cross-references: GB: J03992; NID: g160220; PIDN: AAA29557.1; PID: g160221
A; Cross-references: GB: J03992; NID: g160220; PIDN: AAA29557.1; PID: g160221
                                                                                                                                                                                                                                                                                                             A; Reference number: A54504; A; Accession: A54504
                                                                                                                                                                                                                                                                                                                                                                                                                                                              circumsporozoite protein - Plasmodium malariae (strain Uganda 1-CDC)
C; Species: Plasmodium malariae
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                                                                                                                                                                                      C; Keywords: tander F; 354-407/Domain:
                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Date: 06-Oct-1994 #sequence_revision 04-Nov-1994 #text_change 20-Aug-1999
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395
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                                     1 DIEKKICKMEKCSSVFNVVNS
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57.1%;
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61.9%;
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61.9%;
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415
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                                                                                                                                                                                      type 1 repeat homology
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Pred. No. 8.7e-05;
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Pred. No. 8.3e-05;
                                                                                                   Score 77; DB 2;
Pred. No. 0.00076;
                                                                                 Mismatches
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                                                                                                                                                                                                                                type 1 repeat homology
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A; Molecule type: DNA
A; Residues: 93-485 <LAL>
A; Residues: 93-485 <LAL>
A; Residues: 93-485 <LAL>
A; Cross-references: GB:J03203; NID:g160212; PIDN:AAA29553.1; PID:g160213
A; Cross-references: GB:J03203; NID:g160212; PIDN:AAA29553.1; PID:g160213
C; Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C; Keywords: sporozoite; surface antigen; tandem repeat
E; 1-20/Domain: signal sequence #status predicted <AAT>
E; 21-485/Product: circumsporozoite protein #status predicted <AAT>
E; 21-485/Product: circumsporozoite protein #status predicted <AAT>
E; 21-485/Pregion: 4-residue repeats
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R;di Giovanni, L.; Cochrane, A.H.; Enea, V.
Exp. Parasitol. 70, 373-381, 1990
A;Title: On the evolutionary history of the circumsporozoite protein in plasmodia. A;Reference number: A60610; MUID:90214818
A;Accession: A60610
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C;Date: 17-Apr:1993 #sequence_revision 17-Apr-1993 #text_change
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                                                                                                                                                                                                                                                                                                                                                                        A; Molecule type: DNA
A; Molecule type: DNA
A; Residues: 1-378 <GAL>
A; Residues: 1-378 <GAL>
C; Comment: There are three distinct regions in the mature circumsporozoite protein, the obic membrane-anchoring sequence.
C; Comment: There are 10 tandem copies of a 9-residue repeat (preceded by a 6-residue ind C; Comment: There are 10 tandem protein; thrombospondin type 1 repeat homology
C; Keywords: sporozoite; surface antigen; tandem repeat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       J. Biol. Chem. 263, 5495-5498, 1988
A;Title: Circumsporozoite protein gene fra
A;Reference number: A28615; MUID:88186854
A;Accession: A28615
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A; Residues: 1-485 <DIA>
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A;Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.
A;Reference number: A90889; MUID:87102878
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N;Alternate names: major sporozoite surface antigen
C;Species: Plasmodium cynomolgi
C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
C;Accession: D26255
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Best Local Similarity
"hes 12; Conserv
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F;303-356/Domain:
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Best Local
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     344, DLETEVCTMDKCAGIFNVVSN
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                                                                                                                                     Similarity
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Pred. No.
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C; Accession: A26255
R; Galinski, M.R.; Arnot, D.E.; Cochrane,
Cell 48, 311-319, 1987
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A;Title: The circumsporozoite gene of the Plasmodium cynomolgi complex A;Reference number: A90889; MUID:87102878
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c;Comment: There are 19 tandem copies of a 6-residue repeat and 6 copies of an 11-res
c;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology
C;Keywords: sporozoite; surface antigen; tandem repeat
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C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                obic membrane-anchoring sequence.

C;Comment: There are 16 tandem copies of a 9-residue repeat and 3 copies of a 17-resing comment: There are 16 tandem copies of a 9-residue repeat and 3 copies of a 17-residue 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Title: The circumsporozoite gene of the Plasmodium cynomolgi complex A;Reference number: A90889; MUID:87102878 A;Accession: C26255
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C; Superfamily: circumsporozoite protein; thrombospondin C; Keywords: sporozoite; surface antigen; tandem repeat
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A; Residues: 1-378 <GAL>
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F;20-398/Product: circumsporozoite protein #status predicted <MAT>
F;97-240/Region: 9-residue repeats
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F;323-376/Domain: thrombospondin type 1 repeat homology <THR1>
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Pred. No. 0.0051;
8; Mismatches
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                                                                                                                                       Score 71; DB 1; Pred. No. 0.0054;
                                                                                                      Mismatches
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364 DLETEVCTMDKCAGIFNVVSN

384

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OZZQAC

circumsporozoite protein precursor - Plasmodium cynomolgi (strain Gombak)

N;Alternate names: major sporozoite surface antigen

C;Specles: plasmodium cynomolgi

C;Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 07-Nov-1997

C;Accession: E26255

R;Galinski, M.R.; Arnot, D.E.; Cochrane, A.H.; Barnwell, J.W.; Nussenzweig, R.S.; Enea,

Cell 48, 311-319, 1987

A;Title: The circumsporozoite gene of the Plasmodium cynomolgi complex.

A;Reference number: A90889; MUID:87102878

A;Accession: E26255

A;Molecule type: DNA

A;Residues: 1-401 GGAL>
C;Comment: There are three distinct regions in the mature circumsporozoite protein, the obic membrane-anchoring sequence.

C;Comment: There are 17 tandem copies of the 11-residue repeat D/G-G-A-A-A-G-G-G-N.
C;Superfamily: circumsporozoite protein; thrombospondin type 1 repeat homology

C;Reywords: sporozoite; surface antigen; tandem repeat

F;1-19/Domain: signal sequence #status predicted <SIG>
F;20-401/Froduct: circumsporozoite protein #status predicted <MAT>
F;98-278/Region: 11-residue repeats

F;326-379/Domain: thrombospondin type 1 repeat homology <THR1>
Search completed: January 29, 2002, 10:26:36 Job time: 647 sec
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RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
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RA Cherry J.M., Cawley S., Dahlke C., Davepport L.B., Davies P.,
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RA Dodson K.J., Evangelista C.C., Ferraz C., Ferriera S., Fleischmann W.,
RA Poster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Wei M.-H., Ibegwam C.,
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RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussekrin D.R., Pacleb J.M.,
RA Ralason D.R., Nelson K.A., Nixon K., Nussekrin D.R., Pacleb J.M.,
RA Ralason D.R., Nelson K.A., Sannders R.D. C., Scheeler F., Shen H.,
RA Rimert K., Remington K., Sannders R.D. C., Scheeler F., Shen H.,
Ra Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
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Ephydroidea; Drosophilidae; Drosophila.
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Brown D., Churcher C.M., Barrell B.G., Rajandr Submitted (AUG-1997) to the EMBL/GenBank/DDBJ-i- SIMILARITY: BELONGS TO THE MPP10 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
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FlyBase; FBgn0000158
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                                                                                                                                                                                                                          VD09_VACCV
P04311;
20-MAR-1987
20-MAR-1987
20-AUG-2001
PROTEIN D9.
              between
                                                                                                                                                                                                                                                                                                   VACCV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Appendix to 'The complete DNA sequence of vaccinia vivirology 179:517-563(1990).
-I- SIMILARITY: BELONGS TO THE NUDIX HYDROLASE FAMILY.
                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                             "Nucleotide sequence and g
HindIII D fragment.";
Virology 153:96-112(1986).
-!- SIMILARITY: BELONGS TO
                                                                                                             SEQUENCE FROM N.A.
MEDLINE-86291159; PubMed-3739227;
Niles E.G., Condit R.C., Caro P.,
                                                                                                                                                                                      Vaccinia virus (strain
Viruses; dsDNA viruses,
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MEDLINE-91021027; PubMed-2219722;
                                                                                                                                                                           Orthopoxvirus
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SEQUENCE FROM N.A.
STRAIN-INDIA-1967 / ISOLATE IND3;
STRAIN-19190624; PubMed-8383392;
Shchelkunov S.N., Blinov V.M., Totmenin A.V., Marennil Shchelkunov S.N., Erolov I.V., Chizhikov V.E., Gytorov Kolykhalov A.A., Frolov I.V., Chizhikov V.E., Gytorov Gashikov P.V., Belanov E.F., Belavin P.A., Resenchuk Andzhaparidze O.G., Sandakhchiev L.S.;
"..._`\^+ide sequence analysis of variola virus Hindil
                                                                                                                                                                                                                                                                                                                                                                                                                                           P33070;
01-OCT-1993
01-OCT-1993
20-AUG-2001
PROTEIN D9.
                                                                                                                                                                        STRAIN-INDIA-1967 / ISOLATE IND3;

MEDLINB-93202281; PubMed-8384129;

Shchelkunov S.N., Blinov v.M., Sa

"Genes of variola and vaccinia vi

protective mechanisms.";

PEBS Lett. 319:80-83(1993).
                                                                                                                                                                                                                                                                                                                                                                                                 Variola virus.
Viruses; dsDNA viruses,
Orthopoxvirus.
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InterPro; IPR003300;
Pfam; PF00293; mutT;
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          This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM
                                                    smallpox virus genome.";
Nature 366:748-751(1993)
                                                                                              Knight J.C., Auk
Selivanov N.A.,
                                                                                                                    Massung
                                                                                                                               STRAIN=BANGLADESH-1975;
MEDLINE=94088747; PubMed=8264798;
                                                                                                                                                      SEQUENCE FROM
                                                                                                                                                                                                                                            COMPLETE GENOME
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PROSITE; PS00893;
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                                                                   "Potential virulence determinants smallpox virus genome.";
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                                                                                             g R.F., Esposito J.J., Liu L.,
J.C., Aubin L., Yuran T.E., P
nov N.A., Cavallaro K.F., Kerl
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8; Conservative
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4; Mismatches
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Parsons J.M., Lopar
rlavage A.R., Mahy F
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MEDLIND-97306636; PUDMed-9163903;

MONDAL J., Ortega Perez R., Turian G.;

MOLECULar cloning and expression studies of two divergent alpha-tubulin genes in Neurospora crassa.";

PEMS Microbiol. Lett. 150:33-41(1997);

-1- FUNCTION: TUBULIN IS THE MAJOR CONSTITUENT OF MICROTUBULES.

BINDS TWO MOLES OF GTP, ONE AT AN EXCHANGEABLE SITE ON THE BLOHAL SITE ON THE ALPHA-CHAIN.

CHAIN AND ONE AT A NONEXCHANGEABLE SITE ON THE ALPHA-CHAIN.

-1- SUBUNIT: DIMER OF ALPHA AND BETA CHAINS.
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Microtubules; GTP-binding; Multigene family NP_BIND 142 148 GTP (POTENTIAL)
                                                 PRINTS; PRO1161; TUBULIN.
PRINTS; PRO1162; ALPHATUBULIN.
PROSITE; PS00227; TUBULIN; 1.
                                                                                                                      InterPro; IPR000217; Tubulin.
InterPro; IPR003008; Tubulin_FtsZ
Pfam; PF00091; tubulin; 1.
                                                                                                                                                                                                                                                                      the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Fung1; Ascomycota; Pezizomycotina; Sordariomycetes;
Sordariales; Sordariaceae; Neurospora.
NCBI_TaxID=5141;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; X67119; CAA47598.1; -.
EMBL; X69198; CAA49040.1; -.
EMBL; L22579; AAA60847.1; -.
PIR; F36847; F36847.
PIR; S33113; S33113.
                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
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InterPro; IPR003300; Viral_VD9.
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PIR; S39691; S39691.

Subtilist; BG10582; galr.

InterPro; IPR000880; GalP_UDP_transf.

InterPro; IPR000766; GalP_UDP_transf_II.

Pfam; PF01087; GalP_UDP_transf; 1.

PROSTIE; PS01163; GALP_UDP_TRANSF_II; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glaser P., Kunst F., Arnaud M., Coudart M.P., Gonzald Hullo M.F., Ionescu M., Lubochinsky B., Marcelino L., Presecan E., Santana M., Schneider E., Schweizer J., Rapoport G., Danchin A.;
                                                                                                                      Complete proteome. SEQUENCE 513 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                            "Bacillus subtilis genome project: cloning and sequencing on the region from 325 degrees to 333 degrees."; Mol. Microbiol. 101.371-384(1993).
-i- CATALYTIC ACTIVITY: UTP + ALPHA-D-GALACTOSE 1-PHOSPHATE
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Bacillus/Staphylococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001
                                                                                                                                               Transferase; Nucleotidyltransferase; Galactose metabolism;
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                                                                                                                                                                                                                                                                                                                                                                                                                   UDP-GALACTOSE + PYROPHOSPHATE PATHWAY: GALACTOSE METABOLISM
EKRTITKENVDLVIK 469
                DERTLTKEYEDIVLK 19
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53.3%;
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57.18;
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Last sequence update)
Last annotation update)
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                                                   Score 45; DB Pred. No. 21; 5; Mismatches
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Pred. No. 13;
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                                                                                                                      EBBF2A57A3987532 CRC64;
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21;
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                                                                            Length 513;
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                                                     Indels
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Matches
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Interpro; IPR001241; DNA_topoisoII.
Interpro; IPR002205; DNA_topoisoIV.
Interpro; IPR003594; HATPase_c.
Pfam; PF00204; DNA_topoisoIV; 1.
Pfam; PF00521; DNA_topoisoIV; 1.
Pfam; PF005218; HATPase_c; 1.
                                                                             DOMAIN
DOMAIN
SEQUENCE
                                                                                                                           NP_BIND
ACT_SITE
                                                                                                                                                                                                       SMART; SM00387; HATPASE
SMART; SM00433; TOP2C; I
SMART; SM00434; TOP4C; I
                                                                                                                                                                                                                                                   PRINTS; PRINTS;
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30-MAY-2000
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                                                                                                                 DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    localized DNA topoisomerase II in blot analysis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Komori K., Kuroe K., Yanagisawa K., Tanaka Y.;
"Cloning and characterization of the gene encoding a mitochondrially
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-DEC-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chim. Biophys. Acta 1352:63-72(1997).
FUNCTION: CONTROL OF TOPOLOGICAL STATES OF DNA BY BREAKAGE AND SUBSEQUENT REJOINING OF DNA STRANDS. MAKES DOUBLE-STRAND BREAKS (BY SIMILARITY).
CATALYTIC ACTIVITY: ATP-DEPENDENT BREAKAGE, PASSAG OF DOUBLE-STRANDED DNA.
SUBUNIT: HOMODIMER (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DEVELOPMENTAL STAGE: PRESENT IN GROWTH PHASE AND DURING DEVELOPMENT, ALTHOUGH LEVELS DECLINED AS DEVELOPMENT PROCEEDED SIMILARITY: BELONGS TO THE TYPE II TOPOISOMERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                             European
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                                                                                                                                                                                                                                                                                                                                                                                                                           SWISS-PROT entry is copyright. It is produced through
een the Swiss Institute of Bioinformatics and the EM
European Bioinformatics Institute. There are no restr
NEREDERTLTKEYEDIVLK 19
                                                                                                                                                                                                                           PRO0418; TPI2FAMILY.
PR01158; TOPISMRASEII.
PD000616; DNA_topoisoII;
SM00387; HATPASE_C; 1.
                      Similarity
9; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                     and this statement is not removed
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CLEAVAGE (B
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                                                                                                    Vinals C., de Bolle X.,
Submitted (JAN-1995) to
--- CATALYTIC ACTIVITY:
                                                                                                                                                                                   "D-2-hydroxy-4-methylvalerate dehydrogenase delbrueckii subsp. bulgaricus. II. Mutagenic catalytically important residues.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        coli
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01-MAY-1992 (Rel.
15-JUL-1999 (Rel.
                                    This
                                                                                                                                                                                                                                                                                                                                                                                                       dependent D-lactate dehydrogenase gene in Escherichia coli:purification and characterization of the recombinant enzyme. Biochem. Biophys. Res. Commun. 185:705-712(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Kochhar S., Hunziker P., Leong-Morgenthaler P.M., Hottinger "Primary structure, physicochemical properties, and chemical modification of NAD(+)-dependent D-lactate dehydrogenase. Ev for the presence of Arg-235, His-303, Tyr-101, and Trp-19 at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., MEDLINE-92235079; P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=92008688; PubMed=1915894;
Bernard N., Ferain T., Garmyn D., Hols P., Delcour J.;
"Cloning of the D-lactate dehydrogenase gene from Lactobacillus
delbrueckii subsp. bulgaricus by complementation in Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A. STRAIN=NCIB 11778;
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Garmyn D., Hols P., Cortes A., Clarke A.R., Holbr
                                                                                                                                                                                                                                                                                                           dehydrogenases.";
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                                                                                                                                                                                                                                                                   MUTAGENESIS
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                                                                                                                                                                                                                                                                                                                                                    ochhar S.,
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                                                                                                                                             D-STRUCTURE MODELING.
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Evolutionary relationship of NAD(+)-dependent D-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol.
         s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation European Bioinformatics Institute. There are no restrictions on in
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                                                                DEHYDROGENASES
                                                                               SIMILARITY:
                                                                                          SUBUNIT: HOMODIMER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lett.
                                                                                                                                                                         J. Biochem.
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                                                                                                                                                                                                                                                                   OF HIS-205;
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micutes; Bacillus/Clostridium
                                                                                                                                                                                                                                                                                                                                                                               OTHER
                                                                                                                                                                                                                                                                                                                        comparison of
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SES FAMILY.
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. 22, Last sequence upo
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                                                                                                                                                                        244:213-219(1997).
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                                                                                                                                                                                                                                                                                              Commun. 184:60-66(1992)
                                                                                                    Depiereux E., Feytmans E.;
the EMBL/GenBank/DDBJ databases
D-LACTATE + NAD(+) = PYRUVATE +
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bok J.J., [
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SEQUENCE FROM N.A.
MEDLINE-96257217; PubMed-8666270;
Demers D.M., Metcalf A.E., Talbot P
Demers D.M., Tantar tubulin isoforms
                                                                                                                                                                 15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update
15-JUL-1999 (Rel. 38, Last annotation update
TUBULIN ALPHA-2 CHAIN (ALPHA-II TUBULIN)
                                                                                                                                                                                                  Q94570;
15-DEC-1998
                                                                                                                                 Nephropoidea;
                                                                                                                                       Eumalacostraca; Eucarida;
                                                                                                                                            Homarus americanus (American lobster).
Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
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LeterPro; IPR002162; D_2_hydroxyacid_DH.
Leam; pF00389; 2-Hacid_DH; 1.
ROSITE; PS00065; D_2_HYDROXYACID_DH_1; 1.
ROSITE; PS00670; D_2_HYDROXYACID_DH_2; 1.
ROSITE; PS00671; D_2_HYDROXYACID_DH_3; 1.
                                   FUNCTION:
BINDS TWO
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      BINDS TWO MOLES OF GTP, ONE CHAIN AND ONE AT A NONEXCHAN SUBUNIT: DIMER OF ALPHA AND SIMILARITY: BELONGS TO THE T
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                                                   171:185-191(1996)
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BI; M85224; AAA25246.1; -.
R; S17556; S17556.
R; JN0245; JN0245.
R; A38094; A38094.
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                                           TUBULIN
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61.5%;
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    TO THE TUBULIN
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SUBSTRATE-BINDING ()
BY SIMILARITY
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W: DECREASE OF AC

Q: DECREASE OF AC

Q: DECREASE OF AC

Q: 90% LOSS OF AC

V (IN REF. 1)

> A (IN REF. 1)

> D (IN REF. 1)

> I (IN REF. 1)

> T (IN REF. 1)
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Best Local
                                                             Rieger M., Mueller-Auer S., Brueckner M.;

Rieger M., Mueller-Auer S., Brueckner M.;

Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.

-I FUNCTION: SODIUM EXPORT FROM CELL, TAKES UP EXTERNAL PROTONS I EXCHANGE FOR INTERNAL SODIUM IONS (BY SIMILARITY).

-I SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).

-I SUBCELLULAR LOCATION: THE FUNGAL NA(+)/H(+) EXCHANGER FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAH1_YEAST
Q99271;
Q1-NOV-1997
01-NOV-1997
30-MAY-2000
                                      between
                                                   This
                                                                                                                                                                                                            STRAIN-S288C;
                                                                                                                                                                                                                                                                                              Johnston M., Andrews S., Brinkman R., Cooper J., Ding
Favello A., Fulton L., Gattung S., Greco T., Kirsten J
Hallsworth K., Hawkins J., Hillier L., Jier M., Johnso
Johnston L., Langston Y., Latreille P., Le T., Mardis
                                                                                                                                                                                                                                                                                                                                                                                                                         Saccharomyces cerevisiae
Eukaryota; Fungi; Ascomyc
                                                                                                                                                      SEQUENCE OF 145-985 FROM N.A.
                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                        Miller N., Nhan M., Pauley A., Peluso D., Rifk
Taich A., Trevaskis E., Vignati D., Wilcox L.,
                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C
                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A
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NHA1 OR YLR138W OR L3149 OR L9606.4.
                                                                                                                                                                                   Submitted
                                                                                                                                                                                                                                                                                                                                                                                                             Saccharomycetales;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  YEAST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Microtubules; GTP-binding; Multigene family.

NP_BIND 142 148 GTP (POTENTIAL).

SITE 451 451 INVOLVED IN POLYMERIZATION.

SEQUENCE 451 AA; 50250 MW; 5D7751B2330358E6 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS; PRO1161; TUBULIN.
PRINTS; PRO1162; ALPHATUBULIN.
PROSITE; PS00227; TUBULIN; 1.
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InterPro; IPR003008; Tubulin_Ftsz.
Pfam; PF00091; tubulin; 1.
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                           SWISS-PROT entry is copyright. It is produced through a collaboration en the Swiss Institute of Bioinformatics and the EMBL outstation -
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3; Mismatches
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Best Local S
Matches 9
sequence, expression and mutational analysis transcriptional activator and ARSI-binding pro-
Saccharomyces cerevisiae.";
EMBO J. 8:4265-4272(1989).
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P14164;
01-JAN-1990
01-NOV-1990
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EMBL;
                                                                                                                                                                                                                                                                                                 Science
                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
MEDLINE-90069559; PubMed-2511628;
Diffley J.F.X., Stillman B.;
"Similarity between the transcriptional silencer binding proteins
                                                                     SEQUENCE FROM N.A., AND SEQUENCE OF 120-130 AND SEQUENCE PROMISEDLINE=90076149; PubMed=2686983;
Halfter H., Kavety B., Vandekerckhove J., Kiefer F., Gallwitz Halfter H., Kavety B., Vandekerckhove J., Kiefer F., Gallwitz
                                                                                                                                                             Genes
                                                                                                                                                                                           "The gene encoding ARS-binding factor viability of yeast.";
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=90152338; PubMed=2620828;
Rhode P.R., Sweder K.S., Oegema K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BINDING PROTEIN OBF1).

BAF1 OR ABF1 OR OBF1 OR YKL112W OR YKL505.

Saccharomyces cerevisiae (Baker's yeast).

Eukaryota; Fung1; Ascomycota; Saccharomycotina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1990 (Rel. 16, Last sequence update)
01-FEB-1995 (Rel. 31, Last annotation update)
TRANSCRIPTION FACTOR BAF1 (ARS BINDING FACTOR 1) (PROTEIN ABF1)
(BIDIRECTIONALLY ACTING FACTOR) (SFB-B) (DNA REPLICATION ENHANCER-
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NL; X91258; CAA62653.1;
NL; Z73310; CAA97709.1;
NL; Z73311; CAA97711.1;
NL; Z73311; CAA97711.1;
NHA1.
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IPR000676; NaH_Exchngr.
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. 3:1926-1939(1989).
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I is essential
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EMBL; Z281
EMBL; X775
PIR; S2987
TRANSFAC;
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MEDLINE-92221689; PubMed=1561835;

Jacquier A., Legrain P., Dujon B.;

"Sequence of a 10.7 kb segment of yeast chromosome XI identif

"Sequence of a 10.7 kb segment of yeast chromosome XI identif

APNI and the BAFI loci and reveals one tRNA gene and several

reading frames including homologs to RAD2 and kinases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           reading frames ....
veast 8:121-132(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (Some send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              arrest induced by Kluyveromyces lac
Mol. Cell. Biol. 14:6306-6316(1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Butler A.R., White Stark M.J.R.;
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                                                                                                                                                                                                                                                                           Phosphorylation;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                modified and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The multifunctional protein OBF1 is phosphorylated threonine residues in Saccharomyces cerevisiae."; Proc. Natl. Acad. Sci. U.S.A. 88:4089-4093(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           medLINE=91239512; PubMed=2034654; Francesconi S.C., Eisenberg S.;
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                                                                                                                                                                                                                                                           Trans-acting
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                                                                                                                                                                                                                                                                                                              BL; X16385; CAA34421.1;
BL; X51654; CAA35966.1;
BL; M29067; AAA66311.1;
BL; M63578; AAA34823.1;
BL; S93804; AAB22002.1;
BL; X7511; CAA51951.1;
BL; X7511; CAA54647.1;
R; S29870; S29870.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cell. Biol. 14:6306-6316(1994).

FUNCTION: TRANS-ACTING FACTOR IN THE REGULATION OF TRANSCRIPTION AND IN DNA REPLICATION. INVOLVED IN THE TRANSCRIPTION ACTIVATION OF A SUBSET OF RIBOSOWAL PROTEINS GENES. BINDS THE ARS-ELEMENTS FOUND IN MANY PROMOTERS. BINDS TO THE SEQUENCE 5'-TCN(7)ACG-3'.

SUBCELLULAR LOCATION: NUCLEAR.

PUM: EXTENSIVELY PHOSPHORYLATED ON SER AND THR RESIDUES.

SIMILARITY: STRONG TO KLUYVEROMYCES ABF1, AND LOCAL TO YEAST RAP
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NEEDDVHTQMTKNYSDVV
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                                                                                                                        MW;
                                                                                                                                                                                                                                                                        Activator; DNA-binding; yer; Metal-binding; Zinc;
                                                                                                                     PHOSPHORYLATION (BY PKC) (POP)
H->Q: LOSS OF DNA-BINDING.
C->S: LOSS OF DNA-BINDING.
N-> K (IN REF. 3).
A -> V (IN REF. 3 AND 5).
I -> T (IN REF. 3 AND 5).
TN -> NT (IN REF. 3 AND 5).
TN -> T (IN REF. 3 AND 5).
N-> T (IN REF. 3 AND 6).
N-> T (IN REF. 3 AND 6).
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                                                   Score 43.5; E
Pred. No. 51;
3; Mismatches
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; DNA replication;
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several new
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943 AA

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EMBL; U53877; AAB82375.1; --
EMBL; U53881, AAB82402.1; --
EMBL; X91258; CAA62640.1; --
EMBL; Z73301; CAA97699.1; --
EMBL; Z73302; CAA97700.1; --
EMBL; X95514; CAA61707.1; --
EMBL; X95614; CAA61707.1; --
SGD; S0004119; DIP2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DIP2_YEAST STANDARD;
Q12220; Q05386;
15-JUL-1998 (Rel. 36, Created
15-JUL-1998 (Rel. 36, Last se
15-DEC-1998 (Rel. 37, Last an)
DOM34 INTERACTING PROTEIN 2.
                                                                                                                                                                       PROSITE; PS00678; WD_REPEATS_1; 4.
PROSITE; PS50082; WD_REPEATS_2; 8.
PROSITE; PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                                                                                                                                the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-FY23 / RD005;
Verhasselt P., Voet M., Volckaert G.;
Verhasselt P., Voet M., Volckaert G.;
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: CONTAINS 10 WD REPEATS (TRP-ASP DOMAINS)
-!- SIMILARITY: TO S.FOMBE SPBC3D5.12.
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Johnston M., Andrews S., Brinkman R., Cooper J., Ding H., Du Z., Pulton L., Gattung S., Greco T., Kirsten J., Kucabe Hallsworth K., Hawkins J., Hillier L., Jier M., Johnson D., Johnston L., Langston Y., Latreille P., Le T., Mardis E., Menez Miller N., Nhan M., Pauley A., Peluso D., Rifken L., Riles L., Taich A., Trevaskis E., Vignati D., Wilcox L., Wohldman P., Val
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (JUN-1995) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases.
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Saccharomyces cerevisiae (Baker's yeast).
Succharomyceta; Fungl: Ascomycota; Saccharomycetina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                 Repeat;
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NCBI_TaxID=4932;
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SM00320; WD40;
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7D9AEC7AF6A9C740 CRC64;
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eco T., Kirsten J., Kucaba
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Mardis E., Menezes S.,
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Query Match

Score 43;

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Length 943

Search completed:

January 29,

2002, 11:13:48

Job time:

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Query Match
Best Local Similarity
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Matches 8; Conserv
                                                                                                                                                                                                                                                   InterPro; IPR002136; Ribosomal_L4/L1E. Pfam; PF00573; Ribosomal_L4; 1 Ribosomal protein; rRNA-binding. SEQUENCE 208 AA; 23109 MW; D6D3ECI
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P10135;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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PIR; S02832; R5YM4C.
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MEDLINE=88142549; PubMed
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Bacteria; I
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149 DDQKTLIVTKEKEELVVK 166
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FUNCTION: THIS PROTEIN BINDS DIRECTLY AND SPECIFICALLY TO 23S

RRNA (BY SIMILARITY).
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Firmicutes;
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0901d0 caenorhabd1

096554 cryptospori

096554 cryptospori

096554 cryptospori

057935 cae mays on

057936 pyrococcus

057936 pyrococcus

091552 lactobact

0911q6 campylobact

0911q6 arabidopsis

069068 pseudomonas

091y3 neisseria m

090k9 campylobact

090k9 campylobact

090k9 campylobact

090k9 campylobact

090k9 campylobact

090k0 drosophila

09578 neisseria m

090k0 drosophila

09574 neisseria m

09461 neisseria m

09411 drosophila
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plasmodium
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NCBI_TaxID=5854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ozwara H., Kocken C.H.M., Thomas A.W.;
"Molecular characteristation of erythrocyte binding protein Chimpanzee malaria parasite Plasmodium reichenowi.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AJZ51848; CAB96159.1; -.
InterPro: IFR001596; Pyrophosphatase.
PROSITE; PS00387; PPASE; UNKNOWN_1.
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01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
ERYTHROCYTE BINDING PROFEIN (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 100.0%; Score 96; DB 5; L
Best Local Similarity 100.0%; Pred. No. 1.7e-05;
Matches 19; Conservative 0; Mismatches 0;
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00833
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O9ng63 plasmodium
O9guv9 arabidopsis
O51118 nelsseria m
O9fcr5 nelsseria m
O9fcr5 nelsseria m
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O9exc1 arabidopsis
O91v54 arabidopsis
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9.739 Million cell updates/sec
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                                                                                      January 29, 2002, 11:12:14; Search time 285.36 Seconds
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            GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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                                                                                                                                                                                                                                 473505 seqs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries
                                                              OM protein – protein search, using sw model
                                                                                                                                                                 1 NEREDERTLTKEYEDIVLK 19
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Q05644
Q9NG63
Q9ZUX9
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sp_fungi:*
sp_human:*
sp_invertebrate:*
sp_nammal:*
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.

NCBI_TAXID=3702;
                                                                                                                             STRAIN-FCC1/HN;
Ma C.L., Yu X.B., LI X.R., Shan Z.X.;
Ma C.L., Yu X.B., LI X.R., Shan Z.X.;
"Conservation and antigenicity of erythrocyte binding antigen 175 in plasmodium falciparum isolate FCC1/HN.";
Submitted (AFR-200) to the EMBL/GenBank/DDBJ databases.
EMBL; AF258781; AAR72186.1; --
EMBL; AF258781; AAR72186.1; --
SEDUBNE 1435 AA; 167269 MW; FE958828C7794F22 CRC64;
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SCHRANDEV. COLUMBIA:
Rounsley S.D., Lin X., Kaul S., Shea T.P., Fujii C.Y., Mason T.M.,
Shen M., Ronning C.M., Fraser C.M., Somerville C.R., Venter J.C.;
"Arabidopsis thaliana chromosome II BAC F15K20 genomic sequence.";
Submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AC005824; AAC73022.1;
InterPro; IPR003617; TFS2_N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 50; DB 10; Length 368;
Pred. No. 18;
                                    plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                    Length 1435
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SEOUENCE 368 AA; 42310 MW; 9834AC6EA6C28E12 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-NOV-1996 (TYEMBLEEL. 01, Created)
01-NOV-1996 (TYEMBLEEL. 01, Last sequence update)
01-JUN-2001 (TYEMBLEEL. 17, Last annotation update)
TRANSFERRIN BINDING PROTEIN 2 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAY-1999 (TrEMBLrel. 10, Created)
01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
F15K20.12 PROTEIN.
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ERYTHROCYTE BINDING ANTIGEN 175.
                                                                                                                                                                                                                                                                                  92.7%; Score 89; DB 5; I 94.7%; Pred. No. 0.00018; ative 0; Mismatches 1;
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56.2%;
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 18; Conserv
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                                                                            NCBI_TaxID=5833;
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Q51118;
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                                                                                                                                            SEQUENCE FROM N.A.
MEDILINE-9235776; Pubmed=1496004;
MEDILINE-9235776; Pubmed=1496004;
Adams J.H., Sim B.K., Dolan S.A., Fang X., Kaslow D.C., Miller L.H.;
"A family of erythrocyte binding proteins of malaria parasites.";
Proc. Natl. Acad. Sci. U.S.A. 89:7085-7089(1992).
EMBL; M93397; AAA250600.1;
EMBL; M93397; AAA250600.1;
SEQUENCE 1475 AA; 171487 WW; EE8312823AFF946D CRC64;
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NCBL_TaxID=36329, 5833;
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                                                                                                                                                                                                                                                                                               100.0%; score 96; DB 5; Length 1475; 100.0%; Pred. No. 1.8e-05; Live 0; Mismatches 0; Indels
                                                         plasmodium falciparum.
Eukaryota: Alveolata: Apicomplexa: Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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1421 AA; 165330 MW; 7BE8DDFA07CEE771 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-P. falciparum; STRAIN-ISOLATE 3D7;
Daugherty J.R., Lanar D.E.;
Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
ERYTHROCYTE BINDING ANTIGEN (EBA-175) (FRAGMENT).
               01-NOV-1996 (TrEMBLrel. 01, Last sequence update) 01-NOV-1998 (TrEMBLrel. 08, Last annotation update) ERYTHROCYTE BINDING PROTEIN.
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01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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Mol. Biochem. Parasitol. 60:105-109(1993).

EMBL; U32207; AAA75179.1; -.

EMBL; L07755; AAA02927.1; -.
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Best Local Similarity 94.7
Matches 18; Conservative
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Matches 19; Conservative
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NON_TER 1421 1421
SEQUENCE 1421 AA; 16
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Rokbi B., Renauld-Mongenie G., Mignon M., Danve B., Poncet D., Chabanel C., Caugant D.A., Quentin-Millet M.J.;
"Allelic diversity of the two transferrin binding protein B Gene isotypes among a collection of Neisseria Meningitidis strains representative of serogroup b disease: implication for the composition of a recombinant ThpB-based vaccine.";
                      Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis.
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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MEDLINE-3224009; PubMed-8468000;
Wilton J., Ala'Aldeen D., Palmer H.M., Borriello S.P.;
FEMS Microbiol. Lett. 107:59-66(1993).

EMBL, Y05617; CAA70832.1;
EMBL, X75167; CAA53009.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Rokbi B., Mignon M., Caugant D.A., Quentin Millet M.J.; "Heterogeneity of tbpB, the transferrin-binding protein B gene, am serogroup B Neisseria meningitidis strains of the ET-5 complex."; Clin. Diagn. Lab. Immunol. 4:522-529(1997).
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01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSFERIN BINDING PROTEIN B (TRANSFERRIN-BINDING PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Length 669;
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66;
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68;
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4; Mismatches
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Pred. No. (
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EMBL, AJ279563; CAC05596.1; ...
InterPro; IPR001677; Transferrin_bind.
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Pfam; PF01298; Lipoprotein_5; 1.
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                                                                                                                                                   MEDLINE=20407297; PubMed=10948108;
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                                                                                                                                                                                                                                                                                                                                                                                                                  669 AA; 72161 MW;
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ilarity 50.0%;
Conservative
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Best Local Similarity 50.0
Matches 9; Conservative
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Best Local Similarity
Matches 9; Conserv
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                                                                                                        SEQUENCE FROM N.A.
                                                             NCBI_TaxID-491;
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TBPB OR TBP2.
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STRAIN-9094.
STRAIN-9094.
MEDLINE-2040/1977: PubMed-10948108;
ROKbi B., Renauld-wongenie G., Mignon M., Danve B., Poncet D., Chabanel C., Caugant D.A., Quentin-Millet M.J.;
Allellic diversity of the two transferrin binding protein B Gene isotypes among a collection of Neisseria Meningitidis strains representative of serogroup b disease: implication for the composition of a recombinant Taphe-based vaccine.";
EMBL: AJ279557; CAC05591.1:
InterPo; IPR001677; Transferrin_bind.
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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                                                                               Rokbi B., Maitre-Wilmotte G., Mazarin V., Fourrichon L., Lissolo L., Quentin-Millet M.J.;
"Variable sequences in a mosaic-like domain of meningococcal tbp2
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                                                                                                                                                                                                                                                                                                      217 AA; 22596 MW; 63A98BAA62D70338 CRC64;
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSFERRIN BINDING PROTEIN B (FRAGMENT).
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1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSFERRIN BINDING PROTEIN B (FRAGMENT).
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Pred. No. 66;
4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                     Score 48; DB 2;
Pred. No. 21;
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                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                              encode immunoreactive epitopes.";
FEMS Microbiol. Lett. 132:277-283(1995).
EMBL; X88867; CAA6137.1; -.
InterPro; IPR001677; Transferrin_bind.
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                                                          MEDLINE-96039602; PubMed-7590185;
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50.0%;
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Matches 9; Conservative
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Matches 9; Conserv
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01-MAR-2001
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STRAIN=92123;
MEDLINE=20407297; PubMed=10948108;
MEDLINE=20407297; PubMed=10948108;
Rokbi B., Renauld-Mongenie G., Mignon M., Danve B., Poncet D.,
Rokbi B., Caugant D.A., Quentin-Millet M.J.;
Chabanel C., Caugant D.A., Quentin-Millet M.J.;
"Allelic diversity of the two transferrin binding protein B Gene
isotypes among a collection of Neisseria Meningitidis strains
isotypes among a collection of Naisseria Meningitidis strains
representative of serogroup b disease: implication for the composition
of a recombinant Tbpb-based vaccine.";
Infect. Immun. 68:4938-4947(2000).
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Neisseria meningitidis (serogroup B).
Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
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MEDLINE-20305048; M., Achtman M.;
Linz B., Schenker M., Achtman M.;
"Frequent interspecific genetic exchange between commensal néisseriae
                                                                                                                 Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=487;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Zhu P., Ende A., Brieske N., Morelli G., Popovic T., Riou J.Y., Zhu P., Ende A., Achtman M.; Caugant D.A., Achtman M.; "Microevolution in subgroup III Neisseria meningitidis during three pandemics of epidemic meningitis."; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                      "Clonal groupings associated with successive waves of serogroup meningococcal disease from 1969 to 1997 in Moscow, Russia."; submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                     Achtman M., Ende A., Zhu P., Koroleva I.S., Kusecek B., Morelli
Schuurman I.G.A., Brieske N., Zurth K., Kostyukova N.N.,
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSFERRIN BINDING PROTEIN B (FRAGMENT).
     The control of the co
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Pred. No. 69;
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Mol. Microbiol. 36:1049-1058(2000).
EMBL, AJZ76915, CAC21580.1; -.
InterPro; IPR001677; Transferrin_bind.
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SEQUENCE
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NCBI_TaxID=487;
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Bacteria; Proteobacteria; beta subdivision; Neisseriaceae; Neisseria.
NCBI_TaxID=491;
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Legrain M., Findeli A., Villeval D., Quentin-Millet M., Jacobs E.;
Submitted (AUG-1995) to the EMBL/GenBank/DDBJ databases.
EMBL, 250732; CAA90699.1; -.
Interpro; IPR001677; Transferrin_bind.
Pfam; PF01298; Lipoprotein_5; 1.
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TRANSFERRIN-BINDING PROTEIN 2.
2D1D467569E6A722 CRC64;
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Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
EMBL: X17806; CAC27780.1; ...
SEDUELY X17806; CAC27780.1; ...
SEDUENCE 685 AA; 73775 MW; 30ADB39EF34B31A5 CRC64;
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                                                                                                                                                                                                                              01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSFERRIN BINDING PROTEIN B.
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Pred. No.
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Pred. No.
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517 ERTDEKEIPKEQQDIVYR 534
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               EREDERTLIKEYEDIVLK 19
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Matches 9; Conservative
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01-NOV-1996 (TrEMBLrel.
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689 AA;
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MEDLINE-20305048; PubMed-10844690;
Linz B., Schenker M., Achtman M.;
Linz B., Schenker M., Achtman M.;
"Frequent interspecific genetic exchange between commensal neisseriae
                                                                                                                                                                                                                                     Gaps
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NCBI_TaxID=487;
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Schuurman I.G.A., Brieske N., Zurth K., Kostyukova N.N.,
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SEQUENCE 707 AA; 75729 MW; 9271A060B9DFED04 CRC64;
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01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
TRANSFERRIN BINDING PROTEIN B SUBUNIT (FRAGMENT).
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4; Mismatches
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Mol. Microbiol. 36:1049-1058(2000).
EMBL; AJ27633; CAC21596.1; -.
InterPro; IPR001677; Transferrin_bind.
Pfam; PF01298; Lipoprotein_5; 1.
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Best Local Similarity
Matches 9; Conserv
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SEQUENCE FROM N.A.
STRAIN-Z4311;
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DT 01-JUN-2001 (TrEMBLrel. 17, Created)
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DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GN TRANSFERRIN BINDING PROTEIN B.

OS Nelsseria meningitidis (serogroup B).
OC Bacteria: Proteobacteria: beta subdivision: Nelsseriaceae; Nelsseriaceae; NRL SUBMITTAXID=491;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN-90/94;
RA SUBMITTEG (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RL Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
BR CAC27779-1; -.
SQ SEQUENCE 722 AA; 77921 MW; 0169743E83144B8D CRC64;
SCOUENCE 722 AA; 77921 MW; 0169743E83144B8D CRC64;
SCOUENCE 722 AA; 77921 MW; 0169743E83144B8D CRC64;
SQ SEQUENCE 722 AA; 77921 WW; 0169743E83144B8D CRC64;
SQ SEQUENCE 722 AA; 77921 WW; 0169743E83144BBD CRC64;
SQ SEQUENCE 722 AA; 77921 WW; 0169743E83144BBD CRC64;
SG SEGUENCE 772 AB; 77921 WW; 016974
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Description	Plasmodium falcipa	Band-3 peptide SEO	Recombinant vaccin	Polypeptide antige	Human secreted pro	smq p25A GDP Disso	Human secreted pro	Human colon cancer	Chlamydia trachoma	Human polypeptide	Arabidopsis thalla
SUMMARIES	AAY70297	AAW35494	AAY70278	AAR06991	AAG00310	AAR12388	AAG00240	AAG73892	AAY36933	AAM39296	AAG60904
08	21	18	21	11	21	12	21	22	20	22	21
% Query Match Length DB		σ	350	782	123	447	92	284	283	155	51
% Query Match	100.0	100.0	100.0	100.0	95.1	95.1	87.8	87.8	82.9	80.5	78.0
Score	41	41	41	41	39	39	36	36	34	33	32
Result No.	1	7	e	4	5	9	7	80	6	10	11

Arabidopsis thalia	epitope, P545. multivalent; malaria; vaccine; nic epitope; treatment; ric surface protein 2; SSP-2; e surface protein-1; MSP-1; MSP-2; hrocyte binding antigen-175; RAP-1; gamete specific antigen; -CDC/NIIMALVAC-1 antibody.
AAGG0903 AAGG1365 AAGG9375 AAGG9375 AAGG15329 AAGG59661 AAGG59661 AAGG59962 AAGG59962 AAGG59962 AAGG59962 AAGG59960 AAGG59960 AAGG59960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG5960 AAGG9665	ALIGNMEN AA. LyAC-1; m antigen sporozoite nerozoite ne
22211222222222222222222222222222222222	de; 8 k?/NIMAl. (V) Y) (Y) (Y) (Y) (CSP.) (SA-1; n. SA-1; n. AMA-1.) (Hed professentificevent
552 860 861 862 863 863 864 865 865 865 865 865 865 865 865	ard; peptide; first entry) ciparum RAP-1 ciparum RAP-1 otein; Ctetanus tox te protein; Ctetanus tox tigen-1; LSA-e antigen-1; ry associated asitic; preve ciparum. SASSOCIATE SUBSESSOCIATE SUBSESSOC
7.5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5 5	standard; 00 (first m falciparint protein itope; tet; retrocotice primerane ant mbrane ant thoptry as; tiparasitim falciparinm falciparing 99; 99WO 98; 98US AT INST IMS Shi YP, H. Shi YP, H. Shi YP, H.
011111115555555555555555555555555555555	7. X70297 stu X70297 stu -JUN-2000 asmodium : combinant cell epit cell epit cell epit cell membl ver stage ical me
	RESULT 1 AAY70297 XX AC AAY70297 XX AC AAY70297 XX DT 06-JUN-2 XX DE Plasmodi XX DE Plasmodi XX CITCUMSP KW T-Cell e KW T-Cell e KW T-Cell e KW T-Cell e KW P1927; a XX OS Plasmodi XX VI PR 19-AUG-1 XX PR 21-AUG-1 XX

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The present sequence is the antigenic epitope P545, derived from choptry associated protein-1 (RAP-1) of the asexual blood stage of properly associated protein-1 (RAP-1) of the asexual blood stage of properly decided protein-20 (MITMALVAC-1, which is a multivalent, multistage malarial protein CDC/VAITMALVAC-1, which is a multivalent, multistage malarial cacine or the recombinant protein comprises, melittin signal peptide, vaccine. The recombinant protein comprises, melittin signal peptide, vaccine or ircumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (CSP), sporozoite surface protein-1 (SSP-2), liver stage antigen-1 (CSP), merozoite surface protein-1 (SSP-2), liver stage antigen-1 (CSP), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/VAITMALVAC-1 vaccine has malarial infections. Anti-DCC/VIIMALVAC-1 antibodies can be used for malarial infections. Anti-DCC/VIIMALVAC-1 antibodies can be used for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A non-dendritic peptide carrier (A) has been developed which is coupled through a linker to a solid phase, forming a complex of (A)-solid phase. Where (A) comprises 10-50 amino acids capable of forming a secondary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour; scaffold; inhibition; metastasis; wound healing; solid phase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Non-dendritic peptide carrier linked to a solid phase - useful as a diagnostic agent and as a scaffold for production of chemical
 Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 41; DB 21; Length 8; 100.0%; Pred. No. 4.38+05;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAW35494 standard; peptide; 9 AA.
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                                                                                  Claim 2; Page 17; 52pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   97WO-DE00146
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-APR-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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structure in a benign buffer after liberation from the solid phase, and further the (A)-solid phase complex comprises an immunogenic substance and/or an immune mediator coupled on (A). The present sequence conformation and seample from the present invention. An represents a peptide used in an example from the present invention. An centical derivatives, characterised by covalently attaching molecules at attaching and encorporation into an Immunostimulating Complex (Iscom) resulting and the incorporation into an Immunostimulating Complex (Iscom) resulting or the incorporation into an Immunostimulating Complex (Iscom) resulting complex which is used for the chemical coupling of antigenic (A)-iscom complex which is used for the chemical coupling of antigenic connection peptides having fibronection. Laminin- or vitronectin-like one or more peptides having fibronectin-, Laminin- or vitronectin-like cone or more peptides having fibronectin-, Laminin- or vitronectin-like and for more peptides and push selection of found healing. Also a derivatised (A) can be used and for promotion of specifically-binding aptamers or as a diagnostic contractived from or indicative of pregnancy or of a disease, such as an entity of infantive infantive and income indicative of pregnancy or of a disease, such as an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; apical membrane antigen-1; LSA-1; merozoite surface protein-1; MSP-1; mSP-2; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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23...350
7.1abel= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ;
                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 41; DB 18; Length 9; 100.0%; Pred. No. 4.3e+05; Live 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1..22
/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                       infectious, autoimmune or cancerous disease.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recombinant vaccine CDC/NIIMALVAC-1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70278 standard; Protein; 350 AA.
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Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                     9 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   honey bee
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                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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us-09-763-397a-21.rag

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Human; 5' EST; expressed sequence tag; secreted protein; cDNA isolation; gene therapy; chromosome mapping.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 regulatory sequences and to design expression and secretion vectors.
Gene product may be isolated from a transformed E.coll (*11088) expression system using plasmid pmc9. and may then be used for immunisation against malaria. The product may also be used diagnostically to detect Abs directed against the parasite.
                                                                                                                                                                               Score 41; DB 11; Length 782; Pred. No. 7.2;
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Pred. No. 2.5;
1; Mismatches
                                                                                                                                                                                                                              0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human secreted protein, SEQ ID NO: 4391.
                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG00310 standard; Protein; 123 AA.
                                                                                                                                                                                 Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 8; Conservative 0;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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                                                                                                                 AA;
                                                                                                                                                                                                                                                                                                                   202 ltpleely 209
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                                                                                                                                                                                                                                            The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant protein comprises, melittin signal peptide, (His) 6 tag, T-cell epitope from tetanus toxoid and 21 antigent epitopes from circumsporozoite protein (CSP), sporozoite surface protein-2 (SSP-2), liver stage antigen-1 (LGA-1), merozoite surface protein-1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBB-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of Plasmodium fallciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                            Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 350;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 41; DB 21;
100.0%; Pred. No. 3;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR06991 standard; protein; 782 AA.
                                                                                                                                                                                                    Claim 3; Page 43-44; 52pp; English.
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  Hasnain SE;
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Best Local Similarity 100.

Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum
                                          WPI; 2000-237654/20.
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Shi YP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         350 AA;
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                                                                  N-PSDB; AAZ51336
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-AUG-1989;
14-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-SEP-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP388738-A.
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AAR06991;

AAR06991

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Sequence

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Gaps

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The present sequence is a polypeptide encoded by one of a large number of 5 ESTS derived from mRRAs encoding secreted proteins. The 5 ESTS of 5 ESTS derived from mRRAs encoding secreted proteins. The 5 ESTS of 5 ESTS are derived from 30 Gifferent tissues. EST sequences usually correspond mainly to the 3 of unitranslated region (UTR) of the mRNA because they are often obtained to include of primed CDNA libraries. Such ESTS are not well suited for isolating orDNA sequences derived from the 5' ends of mRNAs and even in the cases where longer CDNA sequences have been obtained, the full 5 of UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' UTR is rarely included. 5' ESTs are derived from mRNAs with intext 5' UTR is rarely used in diagnostic, forensic, gene therapy and chromosome mapping procedures. They are used to obtain upstream chromosome mapping procedures. They are used to obtain upstream croulatory sequences and to design expression and secretion vectors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                       New nucleic acid that is a 5' expressed sequence tag (5' EST) for obtaining cDNAs and genomic DNAs that correspond to 5'ESTs and for diagnostic, forensic, gene therapy and chromosome mapping procedures
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human; colon cancer; colon cancer antigen; diagnosis; detection; colorectal carcinoma; chromosome 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 36; DB 21; Length 92;
Pred. No. 7.2;
2; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human colon cancer antigen protein SEQ ID NO:4656.
                                                      Giordano J;
                                                                                                                                                                                     Claim 13; SEQ ID 4321; 71pp + CD-ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG73892 standard; Protein; 284 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Birse CE,
                                                        Duclert A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            99US-0157137.
99US-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      87.8%;
75.0%;
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99US-0122487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6; Conservative
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                                                          Dumas Milne Edwards J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2001-235357/24.
N-PSDB; AAH33323.
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Best Local Similarity
Matches 6; Conserv
                                                                                         WPI; 2000-500381/45.
                                                                                                                                                                                                                                                                                                                                                                                                                             92 AA;
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46 itpledly 53
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                                                                                                         N-PSDB; AAC00246
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03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
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                                (GEST ) GENSET
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    26-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The protein is a GDP Dissociation Inhibitory Protein (GDI) of molwt. 50-60 {\rm kD} which binds to low mol. wt. 6-protein {\rm smg~p25A}.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                New protein for controlling levels of GTP-binding protein using binding inhibition, by binding to G-protein to inhibit GDP GDP dissociation to GTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
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Pred. No. 9.8;
1; Mismatches
                                                                                                                                                                                                                        smg p25A GDP Dissociation Inhibitory Protein.
                                                                                                                                                                                                                                                   G-protein; Guanosine diphosphate; GDP; GDI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human secreted protein, SEQ ID NO: 4321.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG00240 standard; Protein; 92 AA.
                                                                                                                                     AAR12388 standard; Protein; 447 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 3; Page 1; 12pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 21-FEB-2000; 2000EP-0200610.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      95.1%;
87.5%;
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Matches 7; Conservative
                                                                                                                                                                                                  (first entry)
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N-PSDB; AAQ11984.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 447 AA;
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46 itpleely 53
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                                                      itpleely 53
                                     1 LIPLEELY 8
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AAY36754-Y37949 are encoded by open reading frames (ORFs) of the genome of Chlamydia trachomatis (see AAZ01425). The polypeptides can be used as vaccines against Chlamydia trachomatis. Antisense and ribozyme sequences can also be used to control growth of the microorganism. Chlamydia trachomatis is responsible for a large number of diseases, e.g. eye diseases such as conventional trachoma, nonendemic trachoma, paratrachoma, and inclusion conjunctivitis; genital diseases such as nongonococcal uretritis, epidymitis, cervicitis, sapingitis, and perihepgritis, bartholinitis; pneumopathy in breast feeding infants; and venereal lymphogranulomatosis. The polypeptides of the invention may be of use in treating these diseases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; neuropathy; central nervous system; CNS; Alzheimer's; Parkinson's disease; Hunthington's disease; haemostatic; amyotrophic lateral scleroslis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The invention relates to human nucleic acids (AAI57798-AAI61369) and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ren F, War
                                                                                                                                                                                                                                                             DB 20; Length 283;
59;
                                                                                                                                                                                                                                                                                                               Indels
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Yang Y,
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Xu C, Xue AJ,
R, Drmanac RT;
                                                                                                                                                                                                                                                                          Score 34; DB 2
Pred. No. 59;
1; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM39296 standard; Protein; 155 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human polypeptide SEQ ID NO 2441.
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Wehrman T, Xu
, Goodrich R,
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2000US-0552317.
2000US-0598042.
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2000US-0653450.
2000US-0662191.
2000US-0693036.
                                                                                                                                                                                                                                                                          82.9%;
75.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         26-DEC-2000; 2000WO-US34263
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2000US-0727344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                 6; Conservative
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                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                      283 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (HYSE-) HYSEQ INC.
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Wang Z,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Zhou P,
                                                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAI58452
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09-JUL-2000;
19-JUL-2000;
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19-OCT-2000;
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Wang J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               eukaemia
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                                                                 AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The colon cancer antigens. The colon cancer antigens. The colon cancer antigens have cytostatic activity and can be used in gene therapy and vaccine production. N and P may be used in the prevention, therapy and vaccine production. N and P may be used in the prevention, cancer-sasion. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps. by inserting the nucleic acids into a host cell and culturing the cell to express the proteins. N and P can be used in the prevention, diagnosis and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Vaccine; eye disease; conventional trachoma; nonendemic trachoma; paratrachoma; inclusion conjunctivitis; genital disease; perihepatitis; nongonococcal uretritis; epidymitis; cervicitis; salpingitis; bartholinitis; pneumopathy; venereal lymphogranulomatosis.
 useful for preventing, diagnosing and/or treating colorectal cancers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                              N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present for SEQ ID NO:1027 to 1052, 7921 and 7922.
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Pred. No. 24;
2; Mismatches
                                   Claim 11; Page 6456-6458; 9803pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome sequence of Chlamydia trachomatis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chlamydia trachomatis secreted protein.
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97FR-0015041.
97FR-0016034.
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75.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 75.0°,
6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             07-OCT-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Chlamydia trachomatis.
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                                                                                                                                                                                                                                                                                                                                               present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                      284 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LTPLEELY 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        28-NOV-1997
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Wang D;

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990S-0144085.
990S-0144086.
990S-0144325.
990S-0144331.
990S-0144333.
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990S-0144335.
990S-0144632.
990S-0144884.
990S-0144884.
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99US-0145088.
99US-0145085.
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9905-0137222.
9905-0137502.
9905-0137502.
9905-0138540.
9905-0138647.
9905-0139452.
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99US-0145218
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99US-0143624
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                                               990S-0134941.
990S-0135124.
990S-0135353.
990S-0135629.
990S-0136021.
990S-0136392.
        99US-0134219.
99US-0134221.
99US-0134370:
99US-0134768.
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99US-01
                                                                                                             28-MAY-1999,
    the encoded polypeptides (AAM38642-AAM42213) with nootropic, immunosuppressant and cytostatic activity. The polynucleotides are useful immunosuppressant and cytostatic activity. The polynucleotide or polynucleotide or n gene therapy. A composition containing a polypeptide or polynucleotide of the invention may be used to treat diseases of the peripheral nervous coft the invention may be used to treat diseases of the peripheral nervous coft system, such as peripheral nervous injuries, peripheral nervous such as contains nervous system diseases, such as lateral sclerosis, and Shy-Drager Syndrome. Other uses include the lateral sclerosis, and Shy-Drager Syndrome. Other uses include the cutilisation of the activity, chemotactic/chemokinetic activity, haemostatic cond thrombolytic activity, cancer diagnosis and therapy, drug screening, and thrombolytic activity, arthritis and inflammation, leukaemias and consistence of the screen of the state of the printed specification.
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14-OCT-1999;
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20-AUG-1999;
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The invention relates to human nucleic acids (AAI57798-AAI61369) and
the encoded polypeptides (AAAW8642-AAM42213) with nootropic,
the encoded polypeptides (AAAW8642-AAM42213) with nootropic,
cc the invention may be used to traat diseases of the peripheral nervous
cc f the invention may be used to traat diseases of the peripheral nervous
cc system, such as peripheral nervous injuries, peripheral nervopathy and
csystem, such as peripheral nervous system diseases, such as
localised neuropathies and central nervous system diseases, such as
cc lateral sclerosis, and Shy-Drager Syndrome other uses include the
lateral sclerosis, and Shy-Drager Syndrome other uses include the
cutilisation of the activity, chemotactic/chemokinetic activity, haemostatic
cc attriminibin activity, cancer diagnosis and therapy, drug screening,
and thrombolytic activity, cancer diagnosis and therapy, drug screening,
cc assays for receptor activity, arthritis and inflammation, leukaemias and
cc N.S disorders.
cc specification.
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                                                                                                                                                                                                                                                       Human; nootropic; immunosuppressant; cytostatic; gene therapy; cancer; peripheral nervous system; CNS; Alzheimer's; parkinson's disease; Huntington's disease; haemostatic; amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic; chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel nucleic acids and polypeptides, useful for treating disorders such as central nervous system injuries -
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Yang Y,
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Mismatches
                                                                                                                                          AAM39585 standard; Protein; 76 AA.
                                                                                                                                                                                                                                   Human polypeptide SEQ ID NO 2730.
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25-APR-2000; 2000US-0552317.
09-JUL-2000; 2000US-0598042.
19-JUL-2000; 2000US-062312.
03-AUG-2000; 2000US-0653450.
14-SEP-2000; 2000US-0652191.
19-OCT-2000; 2000US-0653191.
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     Conservative
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N-PSDB; AAI58741.
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          Matches
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76 AA;

Sequence

Length 52;

Query Match Best Local Similarity

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             Query Match 78.0%; Score 32; DB 22; Length 76; Best Local Similarity 75.0%; Pred. No. 36; Matches 1; Indels Matches 1; Indels
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Search completed: January 29, 2002, 10:21:52 Job time: 428,sec

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                                                           US-08-408-604A-32
US-08-408-604A-43
PCT-US93-09626-32
PCT-US93-09626-43
                                                                                                                                                                                                                                                                                                                    ADDRESSEE: Carella, Byrne, Bain, Gilfillan, ADDRESSEE: Cecchi, Stewart & Olstein STREET: 6 Becker Farm Road CITY: Roseland STATE: New Jersey STATE: New Jersey 2IP: 07068
                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Bohinski, Robert J.,
APPLICANT: Whitsett, Jeffrey A.
TITLE OF INVENTION: Nucleic Acid Sequences
TITLE OF INVENTION: Controlling Lung Cell -
TITLE OF INVENTION: Specific Gene Expression
NUMBER OF SEQUENCES: 76
CORRESPONDENCE ADDRESS:
               US-08-477-451-24
US-08-386-727-4
US-08-600-452A-4
US-08-666-271-2
US-08-929-967-8
                                                                                                        US-08-128-971B-14
US-08-408-604A-36
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US-08-805-117-3
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                                                                                                 -08-128-971B-11
                                                                                                                                   US-08-652-877-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/08/442,809A
FILING DATE: 17-MAY-1995
CLASSIFICATION: 536
                                                                                                                                                                                                                   US-08-442-809A-76; Sequence 76, Application US/08442809A; Patent No. 5976873
                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch diskette
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: WordPerfect 5.1 CURRENT APPLICATION DATA:
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MOLECULE TYPE: protein
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GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: SCHRABER, Juergen
APPLICANT: SCHRABER, Juergen
APPLICANT: GOEDECKE, Axel
TITLE OF INVENTION: TREATHENT OF VASCULAR DISORDERS
CURRENT APPLICATION NUMBER: US/09/123,708
CURRENT FILING DATE: 1998-07-28
CURRENT FILING DATE: 1998-07-28
EARLIER FILING DATE: 1998-07-31
EARLIER FILING DATE: 1994-03-31
EARLIER APPLICATION NUMBER: P4411402.8
EARLIER POFICATION NUMBER: P4411402.8
SOFTWARE: PALENTING DATE: 1994-03-31
SOFTWARE: PALENTING DATE: 1904-03-31
SOFTWARE: PALENTING DATE: 1004-03-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 1144;
      ALUNESSEE: Hamilton, Brook, Smith & Reynolds, P.C. STREET: Two Militia Drive CITY: Lexington STATE: Massachusetts
OUNTRY: USA
                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
SOFTWARE: PatentIn DATA:
APPLICATION NUMBER: US/08/319,866
FILING DATE: 7-CCT-1994
CLASSFICATION: 514
PRIOR APPLICATION: 514
APPLICATION NUMBER:
TITLE OF INVENTION: ASSOCIATED WITH LONG-TERM MEMORY NUMBER OF SEQUENCES: 24 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 73.2%; Score 30; DB 2; Lk Best Local Similarity 100.0%; Pred. No. 6.6e+02; Matches 6; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        73.2%; Score 30;
                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Granahan, Particla
REGISTRATION NUMBER: 32,227
REGISTRATION NUMBER: 32,227
REFERENCE/DOCKET NUMBER: CSHL94-03
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 1114 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-009-123-708-2
Sequence 2, Application US/09123708
; Patent No. 6146887
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-319-866-12
                                                                                                                                                                                                             COMPUTER READABLE FORM:
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                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                            APPLICANT: Xie, Qiao-wen
APPLICANT: Nathan, Carl F.
APPLICANT: Mumford, Richard A.
APPLICANT: Calaycay, Jimmy Ramos
TITLE OF INVENTION: DNA Encoding Inducible Nitric Oxide Synthase
NUMBER OF SEQUENCES: 6
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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; Sequence 12, 529223
; Patent No. 529223
; GENERAL INFORMATION: Timothy P. Applicant: Tully, Timothy P. Applicant: Xin, Jerry C. Applicant: Rin, Jerry C. Applicant: Rin, Jerry C. Title OF INVENTION: CLONING AND CHARACTERIZATION OF GENES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 1144;
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                             Score 31; DB 2; Length 371; Pred. No. 1.2e+02;
                                                                            1; Indels
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                                                                                     1; Mismatches
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MEDIUM TYPEE: FLOPPY Disk
COMPUTER: Macintosh Centris550
COMPUTER: Macintosh Centris550
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/147,812
FILING DATE: No. 5766909 Available
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07/841,641
FILING DATE: 02-FEB-1992
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W III
NAME: Wallen, John W III
REGISTRATION NUMBER: 35,403
REGISTRATION INFORMATION:
CHERCOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Merck & Co., Inc.
STREET: 126 East Lincoln Avenue
CITY: Rahway
STATE: New Jersey
                                                                                                                                                                                                                                                                           Sequence 5, Application US/08147812
Patent No. 5766909
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 138825
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1144 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
                                           75.6%;
75.0%;
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Best Local Similarity 100.
Matches 6; Conservative
                             Query Match
Best Local Similarity 75.v.
Best Local Similarity 75.v.
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                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
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| 128 TPLEEL 133
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US-08-319-866-12
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US-08-147-812-5
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Pred. No. 7e+02;
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85.7%; Pred. No. 2.1e+03;
tive 1; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                   2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 6, Application US/08477451
Patent No. 5928865
GENERAL INFORMATION:
APPLICANT: COVACCI, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
                NAME: POOT, Brian W.
REGISTRATION NUMBER: 32,928
REFERENCE/DOCKET NUMBER: 14538A-003710
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 467-9600
FELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1203 amino acids
                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
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NAME: McClung, Barbara G.
REGISTRATION UNDRER: 33,113
REFERENCE/DOCKET UNDRER: 0335.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2708
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 6: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chiron Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STREET: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: CA
COUNTRY: USA
ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                              73.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 3169 amino acids
                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 75.v.
6, Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 73.2
Best Local Similarity 85.77
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MOLECULE TYPE: protein US-08-477-451-6
                                                                                                                                                                                                                                 MOLECULE TYPE: peptide
                                                                                                                                                                                              amino acid
                                                                                                                                                                                                                 linear
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2614 LSPLEEL 2620
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APPLICANT: SCHRADER, Jurgen
APPLICANT: SCHRADION:
APPLICANT: SCHRADION:
APPLICANT: GODGCKE, AACI
TITLE OF INVENTION: TREATMENT OF VASCULAR DISORDERS
FILE REFERENCE: 51169-2004
CURRENT APPLICATION NUMBER: 08/753,503
PRIOR PILING DATE: 1998-03-01
PRIOR PLICATION NUMBER: 08/553,503
PRIOR PLICATION NUMBER: 04/1402.8
PRIOR PLICATION NUMBER: 41/1402.8
PRIOR PLICATION NUMBER: 41/1402.8
PRIOR FILING DATE: 1994-03-31
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn Ver: 2.1
SEQ ID NO 2
LENGTH: 1144
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                                        Gaps
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                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: MILLER, A DUSTY
APPLICANT: WOLCAMOT, GREG
APPLICANT: WOLCAMOT, GREG
APPLICANT: WOLCAMOT, GREG
APPLICANT: WOLCAMOT, LYNN
TITLE OF INVENTION: MUS DUNNI ENDOGENOUS RETROVIRAL
TITLE OF INVENTION: PACKAGING CELL LINES
NUMBER OF INVENTION: ADDRESS:
ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
STREET: TWO EMBARCAGING CENTER, 8th Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/075,272
                  Pred. No. 6.6e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/046,140
FILING DATE: 09-MAY-1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               UMBER: US/09/075,272
08-MAY-1998
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ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
100.08; Pre
                                                                                                                                                                                                             Sequence 2, Application US/09123624 Patent No. 6149936
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 4, Application US/09075272 Patent No. 6136598
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Best Local Similarity 100.
Matches 6; Conservative
                                      6; Conservative
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                  Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                             128 TPLEEL 133
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                                                                         2 TPLEEL 7
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US-09-123-624-2
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APPLICANT: Kramer, Vance C.
APPLICANT: Kramer, Vance C.
APPLICANT: Maderson, Arne R.
APPLICANT: Anderson, Arne R.
APPLICANT: Anderson, Arne R.
APPLICANT: Hart, Hope
APPLICANT: Hart, Hope
APPLICANT: Warren, Greegory W.
APPLICANT: Warren, Jeng S.
APPLICANT: Warren
APPLICANT: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE OF INVENTION: NOVEL INSECTICIDAL TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE TOXINS FROM PHOTORHABDUS LUMINESCENS
TITLE TOXINS FROM 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1; Indels
                                                                                                                                                                                                                                                                     OPERATING SYSTEM: PC-DUS/MS-LUS
SUFTAMER PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/665,647
FILING DATE: 18-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: MUTASHIGE, KateH.
NAME: MUTASHIGE, KateH.
NAME: MUTASHIGE, KateH.
NAME: MUTASHIGE, KateH.
SPEERENCE/DOCKET UNBER: 29,959
REGISTRATION NUMBER: 29,959
REFERENCE/OCKET UNBER: 22,0168
TELEFAX: (202) 827-0168
TELEFAX: (202) 827-0168
TELEFAX: (202) 827-0168
TELEFAX: (202) 827-0168
TELEFAX: 90-4030 MRSNPOERSWSH
TELEX: 90-4030 MRSNPOERSWSH
SEQUENCE CHARACTERICATICS:
2000 Pennsylvania Avenue, NW - Ste. 5500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 70.7%; Score 29; DB 4; I Best Local Similarity 71.4%; Pred. No. 3.3e+02; Matches 5; Conservative 1; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      70.7%; Score 29; DB 2; L
62.5%; Pred. No. 1.9e+02;
Live 2; Mismatches 1;
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US-09-251-645-2
                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09251645; Patent No. 6281413; GENERAL INFORMATION:
                                                                                                                                                                                                    Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 62...
S; Conservative
                                                                              STATE: DC
COUNTRY: USA
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      , MOLECULE TYPE: protein US-08-665-647-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
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311 TPLNDLY 317
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| 150 LDPIKELY 157
                                                  Washingtor
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                    STREET:
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APPLICANT: Dasquez, Nicki J.
APPLICANT: Row, Dorit
APPLICANT: Noronova, Anna F.
APPLICANT: Voronova, Anna F.
APPLICANT: Napolitano, ENTHODS TO
TITLE OF INVENTION: METHODS TO IDENTIFY IMMUNOMODULATORS
TITLE OF INVENTION: USING COGNATE INTERACTION OF PKC-THETA
TITLE OF INVENTION: 89
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.7%; Score 29; DB 3; Length 102; 62.5%; Pred. No. 69;
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                                                                                                                                                                                                                                APPLICANT: Beachy, Philip A.
APPLICANT: Beachy, Jeffrey A.
TITLE OF INVENTON: NOVEL HEDGEHOG-DERIVED POLYPEPTIDES
NUMBER OF SEQUENCES: 109
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINTITE: LEARCESTELL COMPUTER: IBM Competible COMPUTER: IBM Competible SOFTWARE: FastSEQ for Windows Version 2.0b SOFTWARE: FastSEQ for Windows Version 2.0b CURRENT APPLICATION DATA: US/08/946,329A FILING DATE: 07-0CT-1997 PRIOR APPLICATION DATA: PREDICTION NUMBER: 00/061,323 APPLICATION NUMBER: 08/729,743 FILING DATE: 07-0CT-1996 APPLICATION NUMBER: 08/567,357 FILING DATE: 04-DEC-1995 APPLICATION NUMBER: 08/349,498 FILING DATE: 02-DEC-1995 APPLICATION NUMBER: 08/349,498 FILING DATE: 10-DEC-1995 APPLICATION NUMBER: 08/349,498 FILING DATE: 10-DEC-1994 APPORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Fish & Richardson P.C.
STREET: 4225 Executive Square, Suite 1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Halle, Lisa A. REGISTRATION NUMBER: 38,347
REGISTRATION NUMBER: 07265/140001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5099
TELEFAX: 619/678-5099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/08665647 Patent No. 5935803 GENERAL INFORMATION:
                                                                                                                                 US-08-946-329A-93
Sequence 93, Application US/08946329A
Patent No. 6057091
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 619/6/8-5059
INFORMATION FOR SEQ ID NO: 93:
SEQUENCE CHARACTERISCIS:
LENGTH: 102 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 62.5'
Matches 5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 LTTMEEMY 25
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US-08-665-647-7
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Gaps

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GENERAL INFORMATION:
APPLICANT: DELGADO, STEPHEN G.
APPLICANT: DIETRICH, PAUL S.
APPLICANT: FISH, LINDA M.
APPLICANT: HERNAN, RONALD C.
APPLICANT: SANGAMESWARAN, LAKSHMI
TITLE OF INVENTION: SODIUM CHANNEL I-SUBUNIT AND A SPLICE VARIANT THEREOF
NUMBER OF SEQUENCES, 43
CORRESPONDENCE ADDRESS:
ADDRESSEE: JANET PAULINE CLARK
                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 2, Application US/09312183A
Fatent No. 6303766
GENERAL INFORMATION:
APPLICANT: GRABAU, ELIZABETH A.
APPLICANT: HEGEMAN, CARLA E.
TITLE OF INVENTION: SOYBEAN PHYTASE AND NUCLEIC ACID ENCODING THE SAME
FILE REFERENCE: 6617-13
CURRENT APPLICATION NUMBER: US/09/312,183A
NUMBER OF SEQ ID NOS: 24
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 2
LENGTH: 547
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                                                                                                                                                                                                                                   Score 29; DB 4; Length 519;
Pred. No. 4.3e+02;
1; Mismatches 2; Indels
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Pred. No. 4.5e+02;
1; Mismatches 2; Indels
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STREET: 3401 HILLVIEW AVENUE, MS A2-250
CITY: PALO ALTO
STATE: ...
    CURRENT APPLICATION NUMBER: US/09/312,183A CURRENT APPLICATION NUMBER: US/09/312,183A CURRENT FILING DATE: 1999-05-14 NUMBER OF SEQ ID NOS: 24 SOFTWARE: Patentin Ver. 2.1 SEQ ID NO 3 LENGTH: 519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 9, Application US/09024020B
; Patent No. 6030810
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.78;
62.58;
                                                                                                                                                                                                                                   Query Match 70.7%;
Best Local Similarity 62.5%;
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
6617-13
                                                                                                                                 ; TYPE: PRT
; ORGANISM: Glycine max
US-09-312-183A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT
; ORGANISM: Glycine max
US-09-312-183A-2
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224 LTPIHETY 231
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252 LTPIHETY 259
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FILE REFERENCE:
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                                                                                                                           APPLICANT: In M. Whitehead
APPLICANT: Alan Slusarenko
APPLICANT: Duncan Gaskins
APPLICANT: Duncan Gaskins
APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: GUAVA (PSIDIUM GUAJAVA) 13-HYDROPEROXIDE
TITLE OF INVENTION: AYASE AND USES THEREOF
FILE REFERENCE: 06027.0001
CURRENT FILING DATE: 1998-05-13
NUMBER OF SEO ID NOS: 27
SEO ID NO 25
LENGTH: 480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Alan Brash
APPLICANT: Nathalie Tijet
TITLE OF INVENTION: MUSKMELON (CUCUMIS MELO) HYDROPEROXIDE
TITLE OF INVENTION: LYASE AND USES THEREOF
FILE REFERENCE: 06027.0002
CURRENT APPLICATION NUMBER: US/09/537,357
CURRENT FILING DATE: 2000-03-29
NUMBER OF SEQ ID NOS: 56
SOFTWARR: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 29; DB 4; Length 480
Pred. No. 3.9e+02;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; TYPE: PRT
; ORGANISM: Capsicum annum (green pepper)
US-09-537-357-32
                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Capsicum annum (green pepper)
US-09-078-173A-25
                                                                   Sequence 25, Application US/09078173A Patent No. 6200794 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 32, Application US/09537357 Patent No. 6271018 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              70.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 70.7
Best Local Similarity 62:5
Matches 5; Conservative
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Best Local Similarity 62.5
Matches 5; Conservative
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                                                 US-09-078-173A-25
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Pred. No. 1.9e+03;
1; Mismatches 0; Indels
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/024,020B
FILING DATE: 16-FEB-1998
CLASSIFICATION 536
PRIOR APPLICATION DATE: 36
PRIOR APPLICATION DAMBER: US 60/039,447
FILING DATE: 26-FEB-1997
ATTORNEY/AGENT INFORMATION:
NAME: CLARK, JANET P.
REGISTRATION NUMBER: 34,799
REGISTRATION NUMBER: 34,799
REGISTRATION NUMBER: 36,799
FELECOMMULICATION INFORMATION:
TELEFAX: (650) 852-3027
TELEFAX: (650) 852-5322
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE (RARACTERISTICS:
LENGTH: 1976 amino acids
TYPE: Amino acids
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-024-0208-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity 83.3%;
Matches 5; Conservative
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Search completed: January 29, 2002, 10:24:12 Job time: 518 sec

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GDP-dissociation inhibitor XAP-4 - human
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                                                             January 29, 2002, 10:26:47; Search time 144.96 Seconds (without alignments) 4.204 Million cell updates/sec
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 4.5
Compugen Ltd.
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                                                                                                                                                                                         219241 segs, 76174552 residues
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Gencore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                               Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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B69619
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H84729
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137082
A35652
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S38030
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41
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1: pir1:*
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phosphopentomutase	cbs domain protein	CBS domain protein	protein kinase HOG	hypothetical prote	methioninetRNA 1	hypothetical prote	major capsid prote	regulatory protein	VSG expression sit	ESAG 8 protein - T	DNA topoisomerase	valinetRNA ligas	hypothetical prote	probable dGTP pyro	probable homeodoma
JE0180	H72084	н86539	S64950	S46733	S76525	T27457	T13219	BWUT80	A36359	S13724	C70203	S55511	T35218	G71843	E84425
7	7	~	~	~	~	~	~	7	N	7	~	7	7	N	7
393	411	411	435	514	532	532	602	630	630	630	848	1296	133	157	295
78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	78.0	75.6	75.6	75.6
32	32	32	32	32	32	32	32	32	32	32	32	32	31	31	31
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Thoptry-associated protein 1 precursor - malaria parasite (Plasmodium falciparum)
N;Alternate names: protective antigen
S;Alternate names: protective antigen
S;Species: Plasmodium falciparum
C;Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jun-2000
C;Accession: A45514; S27833
R;Aldey, R.G.; Takacs, B.; Lahm, H.W.; Delves, C.J.; Goman, M.; Certa, U.; Matile, H.Wol. Biochem: Parasitol. 41, 125-134, 1990
A;Title: Characterisation and sequence of a protective rhoptry antigen from Plasmodiu
A;Reference number: A45514
A;Accession: A45514
A;Accession: A45514
A;Accession: A45514
A;Residues: 1-782
A;Residues: 1-782
C;Superfamily: Plasmodium falciparum rhoptry-associated protein 1
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Gaps ö Length 782; Indels . 0 2, ö Query Match 100. Best Local Similarity 100. Matches 8; Conservative

ö

DB 2; Score 41; DB Pred. No. 2; ; Mismatches 100.0%; 100.0%; 1111111 202 LTPLEELY 209 œ 1 LTPLEELY

an Xq28 located C;Species: Homo sapiens (man)
C;Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 21-Jul-2000
C;Date: 137082; 139293
R;Sedlacek, Z; Konecki, D.S.; Korn, B.; Klauck, S.M.; Poustka, A.
Mamm. Genome 5, 633-639, 1994
A;Title: Foulutionary conservation and genomic organization of XAP-4, an Xq2
A;Reference number: 137082; MUID:95152170
A;Reference number: 137082

A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Molecule type: DNA
A:Residues: 1-447 <RE2>
A:Cross-freences: EMBL:X79354; NID:g695522; PIDN:CAA55909.1; PID:g695523
A:Accession: I39293
A:Status: preliminary; translated from GB/EMBL/DDBJ

A; Molecule type: mRNA A; Residues: 1-447 <RES> C; Genetics: C; Genetics: EMBL:X79353; NID:g695584; PID:g695585 C; Genetics: GDB:RABGDIA A; Cross-references: GDB:1347097 A; Introns: 15/3; 51/3; 85/1; 130/1; 196/2; 240/2; 273/3; 331/1; 379/2; 397/3

glucokinase (EC 2. hypothetical prote ran GTPase activat

G85699 E64866 S37691

suppressor protein

g Qγ

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R; Nishimura, N.; Nakamura, H.; Takai, Y.; Sano, K.

J. Biol. Chem. 269, 14191-14198, 1994

J. Biol. Chem. 269, 14191-14198, 1994

A; Title. Dictedlar cloning and characterization of two rab GDI species from rat brain
A; Reference number: A54091; MUID:94245743

A; Reference number: A54091; MUID:94245743

A; Status: preliminary
A; Molecule type: mRNA
A; Residues: 1-447 cNIS>
A; Cross-references: GB:X74402

R; Nishimura, N.
Submitted to the EMBL Data Library, July 1993
A; Reference number: S35964
A; Reterence signal array
A; Reference number: S35964
A; Residues: 1-255, D', 257-288, D', 290-447 cNI2>
A; Residues: 1-255, D', 257-288, D', 290-447 cNI2>
A; Residues: 1-255, D', 257-288, D', 290-447 cNI2>
A; Residues: 1-255, D', 290-447 cNI2>
A; Takeyama, Y: Ohmori, T.; Ohyanagi, H.; Saitoh, Y.; Takai, Y.
Biochemistry 30, 909-917, 1991
A; Title: Purification and characterization from rat liver cytosol of a GDP dissociati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   R: McMurray, A.
B: McMurray, A.
B: McMurray, A.
B: McGrence number: 220330
A: Reference number: 220330
A: Reference number: 220330
A: Accession: T27222
A: McGrence: DNA
A: McGrence: Mab.: 299281; PIDN: CAB16511.1; GSPDB: GN00022; CESP: Y57G11C.10
A: Experimental source: clone Y57G11C
C: Genetics:
A: Gene: CESP: Y57G11C.10
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S.Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 26-May-2000
C;Accession: T27222
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A, Molecule type: protein
A, Molecule type: protein
A, Residues: 30-49;104-112;157-186;270-285,'T',287-288,'D',290-293 <UED>
C, Superfamily: human GDP dissociation inhibitor XAP-4
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A;Introns: 332/1; 416/3
C;Superfamily: human GDP dissociation inhibitor XAP-4
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Pred. No. 4.5;
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Pred. No. 2.8;
1; Mismatches
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GDP dissociation inhibitor 2 - mouse
C;Species: Mus musculus (house mouse)
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Best Local Similarity 87.5%;
Matches 7; Conservative
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46 ITPLEELY
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Cyspecies: Rattus norvegicus (Norway rat)
Cyspecies: Rattus norvegicus (Norway rat)
Cyspecies: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 26-May-2000
Cyncession: B56024
RyShisheva A: Suedhof, T.C.; Czech, M.P.
Mol. Cell. Biol. 14, 3459-3468, 1994
A:Title: Cloning, characterization, and expression of a novel GDP dissociation inhibitor
A; Reference number: A56024; MUID:94217740
A; Accession: B56024
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           9
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A;Title: Molecular cloning and characterization of a novel type of regulatory protein A;Reference number: A35652; MUID:90318376
A;Accession: A35652
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-47 < AMR1>
A;Residues: 1-47 < AMR1>
A;Cross.references: GB:D90103; NID:g217563; PIDN:BAA14134.1; PID:g217564; GB:M55560
C;Superfamily: human GDP dissociation inhibitor XAP-4
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N'Alternate names: rab GDI alpha
C;Species: Rattus norvegicus (Norway rat)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-May-2000
C;Accession: A54091; 835964; A37996
                                                                                                                                                                                                                                                                                                                                                                       smg p25A regulatory protein - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 28-Sep-1990 #sequence_revision 28-Sep-1990 #text_change 20-Jun-2000
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A;Molecule type: MRNA
A;Rosidues: 1-447 <SHI>
A;Cross-references: GB:U07952; NID:g493530; PIDN:AAB16909.1; PID:g516540
C;Superfamily: human GDP dissociation inhibitor XAP-4
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Pred. No. 2.8;
1; Mismatches
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                                                    C; Superfamily: human GDP dissociation inhibitor XAP-4
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Pred. No. 2.8;
1; Mismatches
                                                                                                                              DB 2;
                                                                                                                                                                           1; Mismatches
                                                                                                                              Score 39;
Pred. No.
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Best Local Similarity 87.5%;
Matches 7; Conservative 1
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87.5%;
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Matches 7
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Mon Feb

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Cypecies: Drosophila melanogaster
Cybate: 09-bec-1993 #sequence_revision 12-Apr-1996 #text_change 26-May-2000
Cypecies: Drosophila melanogaster
Cybate: 09-bec-1993 #sequence_revision 12-Apr-1996 #text_change 26-May-2000
Rycossion: 35746; 562097; 537806
Rytitle: A Drosophila homolog of bovine smg p25a GDP dissociation inhibitor undergoes
A;Title: A Drosophila homolog of bovine smg p25a GDP dissociation inhibitor undergoes
A;Reference number: 536746; MUID: 93109305
A;Molecule type: mRNA
A;Residues: 1-448 czAH1>
A;Cross-references: EMBL:L03209
A;Accession: 562097
A;Molecule type: protein
A;Residues: 24-47;83-106;'L',230-248;353-383 czAH3>
B;Zahner, J.E.; Cheney, C.M.
Submitted to the EMBL Data Library, March 1993
A;Reference number: 537806
A;Molecule type: mRNA
A;Residues: 1-124', RPWHP', 130-448 czAH2>
A;Cross-references: EMBL:L03209; NID:g157491; PID:g157492
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            A;Cross-references: EMBL:X74401; NID:g396432; PIDN:CAA52412.1; PID:g396433 C;Superfamily; human GDP dissociation inhibitor XAP-4
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                                                                                          Length 445;
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A;Cross-references: FlyBase:FBgn0004868
C;Superfamily: human GDP dissoclation inhibitor XAP-4
                                                                                          Score 36; DB 2;
Pred. No. 12;
2; Mismatches (
                                                                                            87.8%;
75.0%;
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Best Local Similarity
Matches 6; Conserv
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46 ITPLEDLY 53
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47 ITPLEELF 54
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A;Gene: PA3513
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C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 26-May-2000
C;Accession: A56024
E;Sibshava, A.; Suedhof, T.C.; Czech, M.P.
Mol. Cell. Biol. 14, 3459-3468, 1994
A;Title: Cloning, characterization, and expression of a novel GDP dissociation inhibitor A; Reference number: A56024; MUD:94217740
A;Refactus: preliminary
A;Molecule type: mRNA
A;Residues: 1-445 cSHI>
A;Cross-references: GB:U07951
C;Superfamily: human GDP dissociation inhibitor XAP-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Mus musculus (house mouse)
C;Date: 19-Oct-1995 #sequence_revision 19-Oct-1995 #text_change 26-May-2000
C;Accession: C56956
C;Accession: C56956
R;Janoueix-Lerosey, I.; Jollivet, F.; Camonis, J.; Marche, P.N.; Goud, B.
J. Biol. Chem. 270, 14801-14808, 1995
A;Tille: Two-hybrid system screen with the small GTP-binding protein Rab6. Identification.
A;Reference number: A56956; MUID:95301579
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N'Alternate names: rab GDI beta
C.Species: Rattus norvegicus (Norway rat)
C.Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 26-May-2000
C.Accession: B54091; 835965
R.Nishimura, N.; Nakamura, H.; Takai, Y.; Sano, K.
R.Nishimura, N.; Nakamura, H.; Takai, Y.; Sano, K.
A.Fitle: Molecular cloning and characterization of two rab GDI species from rat brain: A.Reference number: A54091; MUID:94245743
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A;Molecule type: mRNA
A;Residues: 1-445 <JAN>
A;Cross-references: GB:L36314; NID:9538410; PIDN:AAA78786.1; PID:9538411
C;Superfamily: human GDP dissociation inhibitor XAP-4
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Pred. No. 12;
2; Mismatches
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12;
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Pred. No.
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GDP dissociation inhibitor beta - mouse
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Best Local Similarity 75.0
Matches 6; Conservative
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Best Local Similarity
Matches 6; Conserv
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46 ITPLEDLY 53
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46 ITPLEDLY 53
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probable hypothetical protein containing obs domains - Chlamydia trachomatis (serotyp probable hypothetical protein containing obs domains - Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Species: Chlamydia trachomatis
C;Stecies: Chlamydia trachomatis
C;Accession: B71538
R;Stephens, R.S.; Kalman, S.; Lammel, C.J.; Fan, J.; Marathe, R.; Aravind, L.; Mitche Science 282, 754-759, 1998
R;Stence 282, 754-759, 1998
A;Title: Genome sequence of an obligate intracellular pathogen of humans: Chlamydia t A;Recession: B71538
A;Accession: B71538
A;Accession: B71538
A;Accession: B71538
A;Accession: B71538
A;Residues: 1-144 - CARN>
A;Molecule type: DNA
A;Residues: 1-414 - CARN>
A;Residues: 1-414 - CARN>
A;Gross references: GB.AE001298; GB.AE001273; NID:g3328659; PIDN:AAC67849.1; PID:g332
A;Genetics:
C;Genetics:
A;Genetics:
A;Genetics:
C;Superfamily: hypothetical protein H10107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   probable receptor protein kinase - rice
C;Species: Oryza sativa (rice)
C;Species: Oryza sativa (rice)
C;Accession: 103784
B;Xu, Y.; Zhu, O; Lamb, C.
Submitted to the EMBL Data Library, June 1995
A;Description: Molecular cloning and characterization of a rice gene encoding leucine
A;Reference number: Z15083
A;Accession: 179784
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Accession: 179784
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-990 cxuy
A;Cross-references: EMBL:X89226; NID:g1263159; PIDN:CAA61510.1
A;Experimental source: cv. IR36, leaf
C;Genetics:
A;Genetics:
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C;Superfamily: protein kinase Xa21; leucine-rich alpha-2-glycoprotein repeat homology
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Pred. No. 75;
1; Mismatches
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Job time: 658 sec
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75.08;
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Best Local Similarity 75.0
Matches 6; Conservative
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213 LTPIENLY 220
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217 LTPLREMY 224
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A;Tille: Evidence for lateral gene transfer between Archaea and Bacteria from genome seq
A;Reference number: A72200; MuID:99287316
A;Status: preliminary
A;Status: preliminary
A;Residues: 1-390
ARRA
A;Residues: 1-390
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A;Residues: 1-390
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A;Residues: 1-390
ARRA
A;Coss references: GB:AE001701; GB:AE000512; NID:94980648; FIDN:AAD35260.1; PID:9498066
C;Genetics:
                                                                                                                                                                                                                                                                                                phosphopentomutase - Thermotoga maritima (strain MSB8)
C;Species: Thermotoga maritima
C;Date: 11-Jun-1999 #sequence_revision 11-Jun-1999 #text_change 21-Jul-2000
C;Accession: E72411
R;Nelson, K.E.; Clayton, R.A.; Gill, S.R.; Gwinn, M.L.; Dodson, R.J.; Haft, D.H.; Hickey Garrett, M.M.; Stewart, A.M.; Cotton, M.D.; Pratt, M.S.; Phillips, C.A.; Richardson, D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 conserved hypothetical protein TCO527 [imported] - Chlamydia muridarum (strain Nigg) conserved hypothetical protein TCO527 [imported] - Chlamydia muridarum (strain Nigg) C; Species: Chlamydia muridarum, Chlamydia trachomatis Moon C; Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 02-Jun-2000 C; Date: 31-Mar-2000 #sead T.D.: Brunham, R.C.; Shen, C.; Gill, S.R.; Heidelberg, J.F.; White, O.; Hickey, C.; Dodson, R.; Gwinn, M.; Nelson, W.; DeBoy, R.; Kolonay, J.; McClarty, G.; Salzberg, Nucleic Acids Res. 28, 1397-1406, 2000 A; Tille: Genome sequences of Chlamydia trachomatis MoPn and Chlamydia pneumoniae AR39, A; Reference number: A81500; MUID:20150255
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A/Molecule Type: DNA
A/Residues: 1-412 <TET>
A/Cross-references: GB.AE002321, GB.AE002160, NID:g7190560, PIDN:AAF39369.1, PID:g719056
A/Experimental source: strain Nigg (MoPn)
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Pred. No. 27;
1; Mismatches 1; Indels
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Score 34; DB 2;
Pred. No. 22;
1; Mismatches
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Pred. No. 28;
1; Mismatches
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C;Superfamily: hypothetical protein H10107
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C; Superfamily: phosphopentomutase
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Best Local Similarity 75.0%;
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Ouery Match
Best Local Similarity 85.7%;
Matches 6; Conservative
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Best Local Similarity 75.0%;
Matches 6; Conservative
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163 IVPLEELY 170
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213 LTPIENLY 220
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MEMG_METCA YZ26_AQUAE Y165_RICPR HOG1_CANAL SELA_HELPY SELA_HELPY SZ200_HUMAN NU62_HUMAN DXS_ECOLI HUTH_HUMAN HUTH_HUMAN

1169 1193 377 386 390 394 5522 619 657 657

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ALIGNMENTS

aquifex aeo rickettsia

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homo sapien
rattus norv
canis famil
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mus musculu
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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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GDIA_CANFA
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GDIB_CANFA
GDIB_HUMAN
GDIB_MOUSE
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Maximum Match 100%
Listing first 45 summaries
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    protein search, using sw model

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Maximum DB seq length: 200000000
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Perfect score:
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saccharomyc saccharomyc synechocyst trypanosoma

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saccharomyc

trypanosoma borrelia bu helicobacte

homo sapien mus musculu

canis famil

saccharomyc feline endo

rattus norv saccharomyc homo sapien methanosarc archaeoglob

P25639 P31792 P78363 P54808

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SEQUENCE OF 349-361
                               Homo sapiens (Human)
                                                                                                                                    SEQUENCE FROM N.A.
                                                     NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        retardation.
                                                                                                               (GDI)
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                                                                                                                                                                                                Canis familiaris (Dog).
Canis familiaris (Dog).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RAB GDP DISSOCIATION INHIBITOR ALPHA (RAB GDI ALPHA) (GDI-1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 39; DB 1; Length 447; Pred. No. 0.82;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                  Score 39; DB 1; Length 447; Pred. No. 0.82;
                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                            10280DAD33E4BCD0 CRC64;
  PRINTS; PRO0891; RABGDIREP.
PRINTS; PRO0892; RABGDI.
GTPase activation; 3D-structure.
SEQUENCE 447 AA; 50565 MW; 69C68B03BDC1BA3F CRC64;
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P31150; P50394;
01-JUL-1993 (Rel. 26, Created)
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87.5%;
                                                    Query Match
Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 8/...
Best Local Similarity 8/...
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ID GDIA_CANFA
AC 097555;
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D'Admo P., Menegon A., Lo Nigro C., Grasso M., Gulisano M., Tamanini F., Bienvenu T., Gedeon A.K., Oostra B., Wu S.-K., Tandon A., Valtorta F., Balch W.E., Chelly J., Toniolo D.; "Mutations in GDII are responsible for X-linked non-specific mental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         VARIANT XLMR PRO-423.
WHEDLINE-98334551; PubMed-9668174;
BIEDLINE-98334551; PubMed-9668174;
BIEDVONU T., Des Portes V., Saint Martin A., McDonell N., Billuart P.,
Carrie A., Vinet M.-C., Couvert P., Toniolo D., Ropers H.-H.,
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                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-95152170; PubMed=7849400;
MEDLINE-95152170; PubMed=7849400;
MEDLINE-95152170; PubMed=7849400;
Sedlacek Z., Konecki D.S., Korn B., Klauck S.M., Poustka A.;
"Evolutionary conservation and genomic organization of XAP-4, an Xq28
located gene coding for a human rab GDP-dissociation inhibitor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nishimura N., Goji J., Nakamura H., Orita S., Takai Y., Sano K.; "Cloning of a brain-type isoform of human Rab GDI and its expression in human neuroblastoma cell lines and tumor specimens."; Cancer Res. 55:5445-5450(1995).
01-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RAB GDP DISSOCIATION INHIBITOR ALPHA (RAB GDI ALPHA) (GDI-1) (XAP-4).
GDI1 OR RABGDIA OR XAP4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "Long-range sequence analysis in Xq28: thirteen known and six candidate genes in 219.4 kb of high GC DNA between the RCP/GCP and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Rasmussen H.H., van Damme J., Puype M., Gesser B., Celis J.E., Vandekerkhove J.; Microsequences of 145 proteins recorded in the two-dimensional protein database of normal human epidermal keratinocytes."; Electrophoresis 13:960-969(1992).
                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bachner D., Sedlacek Z., Korn B., Hameister H., Poustka A.; "Expression patterns of two human genes coding for different dissociation inhibitors (GDIs), extremely conserved proteins in cellular transport."; Hum. Mol. Genet. 4:701-708(1995).
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MEDLINE=96311563; PubMed-8733135;
MEDLINE=96311563; PubMed-8733135;
Chen E.Y., Zollo M., Mazzarella R.A., Ciccodicola A., Chen C.
Zuo L., Heiner C., Burough F.W., Ripetto M., Schlessinger D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (XXX-1992) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hochgeschwender U.;
Submitted (SEP-1994) to the EMBL/GenBank/DDBJ databases
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MEDLINE=98282090: PubMed=9620768;
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MEDLINE=95359978; PubMed=7543319;
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MEDLINE-93162043; PubMed-1286667;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hum. Mol. Genet. 5:659-668(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TISSUE=Retina;
MEDLINE-96062207; PubMed=7585614;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nat. Genet. 19:134-139(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 328-436 FROM N.A.
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                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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NCBI_TaxID=10116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CONFLICT
 RESULT
                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          L -> P (IN XLMR; CAUSES REDUCED BINDING AND RECYCLING OF RAB3A).

FTIG-VAR_008130.

R -> P (IN XLMR).

FTIG=VAR_008131.

D -> G (IN REF. 2).

N -> K (IN REF. 2).

NFD -> GTY (IN REF. 2).
                         ţu
                 -!- DISEASE: DEFECTS IN GDI1 ARE THE CAUSE OF X-LINKED NON-SPECIFIC
                                                                                                                                          MENTAL RETARDATION (XLMR).
Moraine C., van Bokhoven H., Fryns J.-P., Kahn A., Beldjord C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 447;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -> G (IN REF. 4).
-> S (IN REF. 2).
BC283A445E50A652 CRC64;
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H -> Q (IN F
D -> G (IN F
F -> S (IN F
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                                                                                                                                                                                                                                                                                               EWBL; X79355; CAA55909.1; JOINED. EWBL; X79356; CAA55909.1; JOINED. EWBL; X79357; CAA55909.1; JOINED. EWBL; X79359; CAA55909.1; JOINED. EWBL; X79369; CAA55909.1; JOINED. EWBL; X79360; CAA55909.1; JOINED. EWBL; X79361; CAA55909.1; JOINED. EWBL; X79362; CAA55909.1; JOINED. EWBL; X79362; CAA55909.1; JOINED. EWBL; X79363; CAA55909.1; JOINED.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002005; Rab_GDI_REP. Pfam; PF00996; GDI; 1.
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EMBL; U14623; AAA21558.1; --
EMBL; D45021; BAA08078.1; --
EMBL; L05086; AAC15851.1; --
HSSP; P21856; IGND.
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PRINTS; PRO0892; RABGDI.
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Matches 7; Conservative
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36
149
347
409
416
47 AA;
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"Impairment of bile salt-dependent lipase secretion in human pancreatic tumoral SOJ-6 colls.";
J. Cell. Biochem. 79:628-647(2000).
-!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE SUBSEQUENT BINDING OF GTP TO THEM.
                                                                                                                                                                                                                                               Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
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MEDLINE=94245743; PubMed=8188702;
Nishimura N., Nakamura H., Takai Y., Sano K.;
Molecular cloning and characterization of two rab GDI species from Tat brain: brain-specific and ubiquitous types.";
J. Biol. Chem. 269:14191-14198(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -!- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SUBCELLULAR LOCATION: CYTOPLASMIC.
TISSUE SPECIFICITY: HIGH EXPRESSION IN BRAIN, LOWER IN OTHER TISSUES.
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GDIA_RAT STANDARD; PRT; 447 AA.
P50398; Q9R274;
D1-OCT-1996 (Rel. 34, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RAB GDP DISSOCIATION INHIBITOR ALPHA (RAB GDI ALPHA) (GDI-1).
GDII OR RABGDIA.
Rattus norvegicus (Rat).
ENARAYOta; Metazoa; Chordata; Craniata; Vertebrata; Euteleostc Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE-Brain; MEDLINE=94217740; PubMed=7513052; Shisheva A., Suedhof T.C., Czech M.P.; Cloning, characterization, and expression of a novel GDP dissociation inhibitor isoform from skeletal muscle."; Mol. Cell. Biol. 14:3459-3468(1994).
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-> S (IN REF. 2).
-> P (IN REF. 2).
58384671991DF793 CRC64;
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EMBL; AF130987; AAD25536.1;
HSSP; P21856; 1GND.
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PRINTS; PR00892; RABGDI.
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Best Local Similarity <sup>§</sup>
'.hog 7; Conservat
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Gaps

6

Indels

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Mismatches

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Kaibuchi K., Takai Y.;
(APR-1993) to the EMBL/GenBank/DDBJ databases
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46 ITPLEDLY
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               Asada M.,
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SEQUENCE FROM N.A.

Chen W., Feng Y., Chen D., Wandinger-Ness A.;

Chen W., Feng Y., Chen D., Wandinger-Ness A.;

Chen W., Feng Y., Chen D., Wandinger-Ness A.;

Required (for trans-golgi network-to-plasma membrane required for transport and a preferential target for GDP dissociation inhibitor.";

Mol. Biol. Cell 9:3241-3257(1998).

-I-FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB PROTEINS BY INHIBITING THE DISSOCIATION OF GDP FROM THEM, AND THE SUBSEQUENT BINDING OF GTP TO THEM (BY SIMILARITY).

-I-SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                        Canis familiaris (Dog).
Eukaryota, Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 36; DB 1; Length 445; Pred. No. 3.7;
                                                                                                                                                                                                                      20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RAB GDP DISSOCIATION INHIBITOR BETA (RAB GDI BETA) (GDI-2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
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                                                                                                                                                                                 445 AA
                                                                                                                                                                                   PRT;
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HSSP; P21856; 1GND.
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75.0%;
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Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                   STANDARD;
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46 ITPLEDLY 53
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                                      LTPLEELY
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                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                     Sediacek Z., Munstermann E., Mincheva A., Lichter P., Poutska A.; Sediacek Z., Munstermann E., Mincheva A., Lichter P., Poutska A.; "The human rab GDI beta gene with long retroposon-rich introns maps to 10p15 and its pseudogene to 7p11-p13."; Mamm. Genome 9:78-80(1998).
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                                                                                                                                                                                                                                                Caillol N., Pasqualini E., Lloubes R., Lombardo D.; "Impairment of bile salt-dependent lipase secretion in human pancreatic tumoral SOJ-6 cells."; J. Cell. Blochem. 79:628-647(2000).
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Pred. No. 3.7;
2; Mismatches 0; Indels
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CE186A2E3A47FCC9 CRC64;
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EMBL; Y13286; CAA73734.1; --
EMBL; Y13287; CAA73735.1; --
EMBL; Y13289; CAA73735.1; JOINED.
EMBL; Y13289; CAA73735.1; JOINED.
EMBL; Y13291; CAA73735.1; JOINED.
EMBL; Y13291; CAA73735.1; JOINED.
EMBL; Y13293; CAA73735.1; JOINED.
EMBL; Y13293; CAA73735.1; JOINED.
EMBL; Y13295; CAA73735.1; JOINED.
                                                                                                                                                                                                                       TISSUE=Pancreas;
MEDLINE=20453283; PubMed=10996854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002005; Rab_GDI_REP
Pfam; PF00996; GDI; 1.
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SEQUENCE FROM N.A. MEDLINE=98096592; MEDLINE=98096592;
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75.0%;
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PRINTS; PR00891; RABGDIREP.
PRINTS; PR00892; RABGDI.
                                                                                                                                                                                       SEQUENCE OF 81-439 FROM N.A.
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Best Local Similarity 75.0
Matches 6; Conservative
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SEQUENCE 445 AA;
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445 AA; 50537 MW;
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Matches 6; Conserv
                                                                 SEQUENCE FROM N.A.
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46 ITPLEDLY 53
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P50399;
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                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
NCBI_TaxID=10090;
                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GDIC_MOUSE STANDARD; PRT; 445 AA.

Q61588: Q9D8M9;
20-MG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RAB GDP DISSOCIATION INHIBITOR BETA-2 (RAB GDI BETA-2) (GDI-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .;
0
                                               20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
RAB GDP DISSOCIATION INHIBITOR BETA (RAB GDI BETA) (GDI-2).
GDI2 OR RABGDIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                    445 AA; 50512 MW; 7FFD92EAE950EE49 CRC64;
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Pred. No. 3.7;
2; Mismatches
                                                                                                                                                    STRAIN-BALB/C; TISSUE-Skeletal muscle; MEDLINE-94217740; PubMed-7513052;
                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P21856; 1GND.
MGD; MGI:99845; Gdi2.
InterPro: PR002005; Rab_GDI_REP.
Pfam; PF00996; GDI; I.
PRINTS; PR00891; RABGDIREP.
PRINTS; PR00892; RABGDI.
                                             34, Created)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Conservative
                          STANDARD;
                                                                                             Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                            GTPase activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Best Local Similarity
Matches 6; Conserv
                                           01-OCT-1996 (Rel.
                                                                                                                                            SEQUENCE FROM N.A.
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                                                                                                                        NCBI_TaxID-10090;
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46 ITPLEDLY 53
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                          GDIB_MOUSE
P50397;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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GDIC_MOUSE
                 GDIB_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                       RA Arakwa T., Hara A., Shibata K., Yoshino M., Itoh M., Ishli Y.,
RA Arakwa T., Hara A., Shibata K., Yoshino H., Adachi J., Fukuda S.,
RA Arakwa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Rochiwa H.,
RA Schriml L.M., Staubli F., Sizuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Oustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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MEDLINE-95301579; PubMed-7782346; Janoueix-Lerosey I., Jollivet F., Camonis J., Marche P.N., Goud B.; Janoueix-Lerosey I., Jollivet F., Camonis J., Marche P.N., Goud B.; "Two-hybrid system screen with the small GTP-binding protein Rab6. Identification of a novel mouse GDP dissociation inhibitor isoform and two other potential partners of Rab6."; J. Biol. Chem. 270:14801-14808(1995).
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--- SIMILARITY: BELONGS TO THE TCD/MRS6 FAMILY OF GDP DISSOCIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 409:685-690(2001).

-!- FUNCTION: REGULATES THE GDP/GTP EXCHANGE REACTION OF MOST RAB PROTEINS BY INITIATING THE DISSOCIATION OF GDP FROM THEM, AND SUBSEQUENT BINDING OF GTP TO THEM.

-!- SUBSECLLULAR LOCATION: CYTOPLASMIC AND MEMBRANE-ASSOCIATED (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayashizaki Y.; "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      I -> N (IN REF. 2).
483B7C7456B30525 CRC64;
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01-OCT-1996 (Rel. 34, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                     STRAIN-C57BL/6J; TISSUE-Pancreas;
MEDLINE-21085660; PubMed-11217851;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; P21856; IGND.
MGD; MGI:105939; Gdi3.
InterPro; PFR005005; Rab_GDI_REP.
PEnm; PFR00996; GDI; DRINTS; PR00891; RABGDIREP.
GTPase activation.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AK007871; BAB25321.1; -.
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Submitted (JUL-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Methanococcus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     YA58_METJA
                                                                                                                                                                                                                                                                                                               SEQUENCE
                                                                                                                                                                                                                                                                                              CONFLICT
                                                                                                                                                                                                                                                                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                             058458:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MJ1058
                                                                                                                                                                                                                                                                                                                                                                                                                                             YAS8_METJA
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                                                                                                                                                                                                                                                                                                                                                                                     Qγ
                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its mose by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb.sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                                                                                    Gaps
                                                  Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Rattus.
                                                                                                 STRAIN-SPRAGUE-DAMLEY, TISSUE-Brain;
MEDLINE-94245743; PubMed-8188702;
Nishimura N., Nakamura H., Takai Y., Sano K.;
Nishimura A., Nakamura H., Takai Y., Sano K.;
Molecular cloning and characterization of two rab GDI species from rat brain-specific and ubiquitous types.";
J. Biol. Chem. 269:14191-14198(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
0
           15-JUL-1998 (Rel. 36, Last annotation update)
RAB GDP DISSOCIATION INHIBITOR BETA-2 (RAB GDI BETA-2) (GDI-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01.NOV-1995 (Rel. 32, Created)
01.NOV-1995 (Rel. 32, Last sequence update)
20.AUG-2001 (Rel. 40, Last annotation update)
PHOSPHOPENTOMUTASE (EC 5.4.2.7) (PHOSPHODEOXYRIBOMUTASE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 445;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                  D081ABB31DB9CD29 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group;
Bacillus/graphylococcus group; Bacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-BR151;
Schuch R., Piggot P.J., Garibian A., Nygaard P.;
                                                                                                                                                                SEQUENCE OF 30-54 AND 58-74, AND CHARACTERIZATION. MEDLINE-95298038; PubMed=7779099;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 36; DB 1;
Pred. No. 3.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           396 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                  InterPro; IPR002005; Rab_GDI_REP. Pfam; PF00996; GDI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     445 AA; 50685 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 87.8%;
75.0%;
                                                    Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                EMBL; X74401; CAA52412.1; -. HSSP; P21856; 1GND.
                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0891; RABGDIREP. PRINTS; PR00892; RABGDI. GTPase activation. SEQUENCE 445 AA; 50685 M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ouery Match
Best Local Similarity 75.0
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                               Rattus norvegicus (Rat)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacillus subtilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1423;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    :||||:||
46 ITPLEDLY 53
                                                                                               SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LTPLEELY 8
                                                                            NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                     INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DEOB_BACSU
ID DEOB_BACSU
AC P46353;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SECUENCE FROM N.A.

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

STRAIN=JAL-1 / DSM 2661 / ATCC 43067;

MEDLINE=9633799; PubMed=8688087;

Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,

Bult C.J., White O., Olsen G.J., Zhou L., Clayton R.A., Goodyne J.D.,

Sutton G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Goodyne J.D.,

Kerlavage A.R., Doughberty B.A., Tomb J.-F., Adams M.D., Reich C.I.,

Voverbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,

Scott J.L., Geodyngen N.S.M., Weidman J.F., Fuhrmann J.L., Nauyen D.,

Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borrodovsky M.,

Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;

"Complete genome sequence of the methanogenic archaeon, Methanococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                         5-PHOSPHATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ;
                         Archaea; Euryarchaeota; Methanococcales; Methanococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 1; Length 396;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Indels
                                                                                                                                                       M -> L (IN REF. 2).
MISSING (IN REF. 2).
E -> G (IN REF. 2).
; C41A3BEE4317456E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Science 273:1058-1073(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 609 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pred. No. 14;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 33;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Subtilist; BG11331; drm.
Subtilist; BG11331; drm.
InterPro; IPR002599; Metalloenzyme.
Pfam; PF01676; Metalloenzyme; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                44294 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U32685; AAA74433.1; -.
EMBL; D84432; BAA12650.1; -.
EMBL; Z99116; CAB14282.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Isomerase; Complete proteome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Last a
HYPOTHETICAL PROTEIN MJ1058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methanococcus jannaschii.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             78
210
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
6, Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      318 3
396 AA;
SEQUENCE FROM N.A. STRAIN=168 / JH642;
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169 VVPLEELY 176
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NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-YNN 295;
                                                                                                                                                                                                                                |||||||
| 122 PLEELY 127
                                                                                                                                                                                                                  3 PLEELY 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-GRE88;
                                                                                                                                                                                                                                                                                              SD22_YEAST
P36047;
                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                    SD22_YEAST
                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                       qq
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                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                             01-FEB-1991 (Rel. 17, Created)
01-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EUKARYOTIC TRANSLATION INITIATION FACTOR 2 ALPHA SUBUNIT (EIF-2-
                                                                                                                                                                                                                                                                                                                                                                                   SUIZ OR TIF211 OR VJR007W OR J1429.
Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIINE=89202411; PubMed=2649894; Cigan A.M., Pablich E.K., Feng L., Donahue T.F.; Cigan A.M., Pablich E.K., Feng L., Donahue T.F.; "reast translation initiation suppressor sui2 encodes the alpha subunit of eukaryotic initiation factor 2 and shares sequence identity with the human alpha subunit."; Proc. Natl. Acad. Sci. U.S.A. 86:2784-2788(1989).
                                                                                                                                                                                                        .;
0
                                                                                                                                                                                 ; DB 1; Length 609; . 23;
                                                                                                                                                                                                        1; Indels
                                                                                                             InterPro; IPR003696; Carbamoyltransferase.
Pfan, PR02543; CncH.Modu; 1.
Hypothetical protein; Transferase; Complete proteome.
SEQUENCE 609 AA; 71733 MW; C91899CF01CB84EA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    -1- SIMILARITY: BELONGS TO THE EIF-2-ALPHA FAMILY.
                                                                                                                                                                                                                                                                                                          304 AA
                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                 Score 33;
Pred. No.
                                                                                                                                                                                                      ;
                                                                                                                                                                                 80.5%;
85.7%;
                                                                                        EMBL; U67549; AAB99062.1; -.
                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
STRAIN-S288C / FY1679;
                                                                                                                                                                                Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                        359 TPFEELY 365
                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=4932;
                                                                                                                                                                                                                           2 TPLEELY 8
                                                                                                     FIGR; MJ1058
                                                                                                                                                                                                                                                                                                        IF2A_YEAST
P20459;
                                                                                                                                                                                                                                                                                                                                                                             ALPHA)
                                                                                                                                                                                                                                                                                              IF2A_YEAST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -!- FUNCTION: POTENTIAL REGULATOR OF THE MITOTIC FUNCTION OF YEAST TYPE 1 PROTEIN PHOSPHATASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Maia E Silva A., Bossier P., Vilela C., Fernandes L., Soares H., Guerreiro P., Rodrigues-Pousada C.;
Submitted (MAR-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -i- SUBCELLULAR LOCATION: NUCLEAR (BY SIMILARITY).
-i- SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS (LRR).
-i- SIMILARITY: STRONG, TO S.POMBE SDS22 AND C.ELEGANS T09A5.9.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-93348778; PubMed-8394042;
Cheret G., Mattheakis L.C., Sor F.;
I-DNA sequence analysis of the YCN2 region of chromosome XI in
Saccharomyces cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                               78.0%; Score 32; DB 1; Length 304; 100.0%; Pred. No. 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mackelvie S.H., Andrews P.D., Stark M.J.R.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                 PHOSPHORYLATION (BY GCN2)
AF4F1C80303A4E98 CRC64;
                                                                                                                                                                                                                                                                    Initiation factor; Protein biosynthesis; RNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomycetales; Saccharomycetaceae; Saccharomyces
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-1994 (Rel. 29, Created)
01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 40, Last annotation update)
PROTELN PHOSPHAMASES PPI REGULATORY SUBUNIT SDS22.
SDS22 OR EGP1 OR YKL193C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Saccharomyces cerevisiae (Baker's yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL: X83609; CAA58588.1; -.
EMBL: 228193; CAA82037.1; -.
EMBL: X69765; -: NOT_ANNOTATED_CDS.
PIR: S38030; S38030.
                                                                                                                                                                                                                                                                                                                                                                   34717 MW;
          :::
EMBL, M25552, AAA70332.1; --
EMBL, X87611; CAA60929.1; --
EMBL, Z49507; CAA69529.1; --
PIR; A32108; A32108.
SGD; S0007767; SU12.
Interpro; IPR003029; S1.
Pfam; PF00575; S1; 1.
SWART; SM00316; S1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE OF 1-136 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yeast 9:661-667(1993)
                                                                                                                                                                                                                                                                                                Phosphorylation.
MOD_RES 52
SEQUENCE 304 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Best Local Similarity
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or send an email to license@isb-sib.ch).
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Best Local Similarity
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                          298 TPLSELY 304
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NCBI_TaxID=4896;
                                                                                                                                                                                                                                                                                                                                                                                  2 TPLEELY 8
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P41391;
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RMAL_SCHPO
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I-SIMILARITY: BELONGS TO THE DIHYDROXYACETONE KINASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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STRAIN-RIL / MG1655;
MEDLINE-974667; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Blattner F.R., Glado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 39.5 KDA PROTEIN IN TREA-PTH INTERGENIC REGION.
YCGT OR B1200.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 32; DB 1; Length 338; Pred. No. 20; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                             1EF434C7276ABAEA CRC64;
                                                                                                                                                                                         Nuclear protein.
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                                                                                                                                                                                         Mitosis;
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LERR 3.
LERR 4.
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LERR 7.
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SGD; S0001676; SDS22.
InterPro; IPR001611; LRR.
InterPro; IPR003592; LRR_out.
Pfan; PF00560; LRR; 9.
PRINTS; PR00019; LEUKICHRPT.
SMART; SM00370; LRR; 11.
I-aucine-rich repeat; Repeat; Mi
                                                                                                                                                                                                                                                                                                                                                                                                                                                 38887 MW;
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112
113
1136
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202
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270
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REPEAT 65 8
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156
181
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246
295
338 AA;
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Best Local Similarity
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P76015:
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This SWISS-PROT entry is copyright. It is produced through a collaboration
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Mol. Cell 3:781-791(1999),
-1- FUNCTION: GIPASE ACTIVATOR FOR THE NUCLEAR RAS-RELATED REGULATORY
PROTEIN SPIL (RAN), CONVERTING IT TO THE PUTATIVELY INACTIVE GDP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "STRAIN-972;
Devlin K., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                             Gaps
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MEDLINE-99322670; PubMed-10394366;
Hillig R.C., Renault L., Vetter I.R., Drell T. IV, Wittinghofer A.,
Becker J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bischoff F.R., Krebber H., Kempf T., Hermes I., Ponstingl H.; "Hunan RanGTPBese-activating protein RanGAPD is a homologue of yeast Rnalp involved in mRNA processing and transport."; proc. Natl. Acad. Sci. U.S.A. 92:1749-1753(1995).
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-!- SIMILARITY: CONTAINS 8 LEUCINE-RICH REPEATS (LRR).
-!- SIMILARITY: TO MAMMALIAN RANGAPI.
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MEDLINE-93385646; PubMed-8374168;
MEDLINE-93385646; PubMed-8374168;
MAICHIONE MONGLOQUE OF THE RNAI gene product in
"A functional homologue of the RNAI gene product in
Schizosaccharomyces pombe: purification, biochemical
characterization, and identification of a leucine-rich repeat
                                                                                                                                                                                                                  Score 32; DB 1; Length 366;
Pred. No. 22;
EMBL; AE000218; AAC74284.1; -.
EMBL; D90754; BAA36097.1; -.
ECOGENE; EG13901; YC9T.
Hypothetical protein; Complete proteome.
SEQUENCE 366 AA: 39494 MW; 08EA76FC216E55FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-ANG-2001 (Rel. 40, Last annotation update)
RNAI OF SPAC22E12.07.
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SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
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between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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LRR 2.
LRR 3.
LRR 4.
LRR 6.
LRR 6.
LRR 7.
LRR 8.
ASP/GLU-RICH (ACIDIC).
CRITICAL RESIDUE FOR GTP HYDROLYSIS.
                                                                                                                                                                                                           Leucine-rich repeat; 3D-structure.
                                                                                                                                                                                                                                                                                                                                                                                                  Score 32; DB 1; Length 386;
Pred. No. 23;
0; Mismatches 1; Indels
                                                                                       EMBL; X69882; CAA49509.1; EMBL; Z70043; CAA93894.1; PBB; 17K6; 29-MAR-00.
INCEPPO: IPR001611; LRR.
INTERPO: IPR001611; LRR.
INTERPO: IPR003592; LRR_out.
SAART; SWOO370; LRR; 5.
GTPASE ACLIVATION; Repeat; Leuc REPEAT 83 112 LR REPEAT 113 141 LR REPEAT 113 141 LR REPEAT 113 141 LR REPEAT 1179 206 LR
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053053 listeria iv
P95904 sulfolobus
099x76 staphylococ
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097845 saccharomyc
04885 arabidopsis
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O9hy96 pseudomonas
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Ogpkd8 chlamydia m
O84258 chlamydia t
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STRAIN=SIBRRA LEONE;
MEDLINEP-9329317; PubMed-7685740;
Howard R.F., Jensen J.B., Franklin H.L.;
Reactivity profile of human anti-82-kilodalton rhoptry protein antibodies generated during natural infection with Plasmodium falciparum.";
EMBL; L10322; AAB59202.1; -.
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NCBL_TaxID-5833;
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llarity 100.0%; Pred. No. 1.2;
Conservative 0; Mismatches
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Q9VLB7
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Q40699
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Q48852
Q9SKY2
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Q9KCN9
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STRAIN-SIERRA LEONE;
MEDLINE-92244303; Pubmed-1574089;
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Q26002;
01-NOV-1996 (TEMBLIEL 01, C
01-NOV-1998 (TEMBLIEL 08, I
01-NOV-1998 (TEMBLIEL 08, I
RHOPIRY PROTEIN (FRAGMENT).
  Plasmodium falciparum
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Q25730 plasmodium
Q26104 plasmodium
Q26007 plasmodium
Q20431 plasmodium
Q9u431 plasmodium
Q9u429 plasmodium
Q9u414 geodia cydo
Q21449 caenorhabdi
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Compugen Ltd.
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                 GenCore version Copyright (c) 1993 - 2000
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NCBI_TaxID=5854;
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                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5837;
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                                                                                           Length 292;
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Shi Y., Lal A.A.; Shi Y., Lal A.A.; Shi Y., Lal A.A.; Shi Y., Lal A.A.; Submitted (FBA-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20986; AAA63682.1; -.
SEQUENCE 782 AA; 90160 MW; DE6D1BE2FAC308A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0; Indels
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Shi Y., Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20985; AAA63681.1; -.
SEQUENCE 782 AA; 90023 MW; F69E26A2A564C8EA CRC64;
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                                                      A35C979C3FEC3019 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 14, Last annotation update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAR-2001 (TrEMBLrel. 16, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN-1.
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100.0%; Score 41; DB 5
Best Local Similarity 100.0%; Pred. No. 2.2;
Matches 8; Conservative 0; Mismatches
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Mol. Biochem. Parasitol. 77:95-98(1996).

EMBL: U41074; AAC47090.1; -.
NON_TER 22 292
SEQUENCE 292 AA; 32345 MW; A35C979C3
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Best Local Similarity 100.
Matches 8; Conservative
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Best Local Similarity 100.
Matches 8; Conservative
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202 LTPLEELY 209
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Mol. Biochem. Parasitol. 51:327-330(1992).
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Mol. Biochem. Parasitol. 51:327-330(1992).
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SEQUENCE FROM N.A.
STRAIN-INDD (INDIAN ISOLATE D);
STRAIN-INDD (INDIAN ISOLATE D);
MEDLINE-96379224; Pubmed-8784775;
Howard R.F., Peterson C.;
"Limited Rap-1 sequence diversity in field isolates of Plasmodium falciparum.";
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN=TANZANIA I/CDC;
MEDLINE=93293317; PubMed=7685740;
Howard R.F., Jensen J.B., Franklin H.L.;
Reactivity profile of human anti-82-kilodalton rhoptry protein antibodies generated during natural infection with Plasmodium falciparum.;
Infect. Immun. 61:2960-2965(1993).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
STRAIN INDD RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
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171 AA; 18531 MW; 192CBAFC68970CB8 CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
RHOPTRY PROTEIN (FRAGMENI).
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STRAIN-INDD (INDIAN ISOLATE D);
MEDLINE-92244303; PubMed=1574089;
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EMBL; L10323; AAA29742.1; -.
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STRAIN=TANZANIA I/CDC;
MEDLINE=92244303; PubMed=1574089;
Howard R.F.;
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Matches 8; Conservative
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NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY -ASSOCIATED PROTEIN 1 (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
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iive 0; Mismatches 0;
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Q9U431;
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"Characterisation and sequence of a protective rhoptry antigen from Plasmodium falciparum.";
Mol. Blochem. Parasitol. 41:125-134(1990).
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           two Plasmodium falciparum isolates.";
Mol. Blochem. Parasitol. 51:327-330(1992).
EMBL: M60807; AA:29717.1; -
SEQUENCE 782 AA: 90096 MW; DIAD099862528D42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         782 AA; 90080 MW; 2F2E240D40A4C902 CRC64;
                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-3UN-2000 (TrEMBLrel. 14, Last annotation update)
PR66 RHOPTRY PRECURSOR PROTEIN.
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EMBL; M32853; AAA29753.1; -.
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STRAIN-HONDURAS I CDC;
MEDLINE-90348711; PubMed-2200961;
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STRAIN-HONDURAS I CDC;
MEDLINE-92244303; PubMed-1574089;
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Best Local Similarity 100.
Matches 8; Conservative
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202 LTPLEELY 209
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RESULT Q26007

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SEQUENCE FROM N.A. Sediacek Z., Shimeld S.M., Muenstermann E., Poustka A.; Sediacek Z., Shimeld S.M., Muenstermann E., Poustka A.; Sediacek Z., Shimeld S.M., Muenstermann E., Poustka A.; The amphioxus RAB gdp-dissociation inhibitor (GDI) gene is neural-special implications fort the evolution of function of chordate RAB GDI genes."; Submitted (DEC-1998) to the EMBL/GenBank/DDBJ databases.
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NCBI_TaxID=6239;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 39; DB 5; Length 446; Pred. No. 8.9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mcmurray A.;
Submitted (SEP-1997) to the EMBL/GenBank/DDBJ databases.
Submitted (O0002; AAA17051.1; -..
EMBL; 299281; CAB16511.1; -..
HSSP; P21856; 1GND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
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Submitted (APR-1993) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Interpro; IPR002005; Rab_GDI_REP.
Pfam: PR00996; GDI; 1.
PRINTS; PR00991; RABGDIREP.
SEQUENCE 444 AA, 50025 MW; 0F3CFC46B75161DD CRC64;
                                                                                                                                                                                EMBL. Y18521; CAB46230.1; -.

EMBL. Y18521; CAB46230.1; -.

InterPro; IPR003006; Ig_MHC.

InterPro; IPR002005; Rab_GDI_REP.

Pfam; PR00996; GDI; 1.

PROSITE; PS00290; IG_MHC; UNKNOWN_1.

SEQUENCE . 446 AA; 49759 MW; 69256AFFC0188D3A CRC64;
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Last annotation update)
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RABGDI PROTEIN.
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04,
17,
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Best Local Similarity 87.5%;
Matches 7; Conservative
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Best Local Similarity 87.5.
Best Local 7; Conservative
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SEQUENCE FROM N.A.
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46 ITPLEELY 53
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NCBI_TaxID=7739;
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Q21449
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                                                                                                                                                                                                                                                                                                                                                                          Saul A.; "Efficacy of vaccines containing Rhoptry-Associated Proteins RAP1 and RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF205284; AAF23405.1; SEQUENCE 782 AA; 90041 MW; 27F2EA9BC930434E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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Eukaryota; Metazoa; Chordata; Cephalochordata; Branchiostomidae;
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NCBL_TaxID=5833;
                                                                                                                                                                                          Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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STRAIN=FCC1/HN;
Li X.R., Luo S.H., Yu X.B., Shan Z.X., Ma C.L.;
Li X.R., Luo S.H., Yu X.B., Shan Z.X., Ma C.L.;
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF206631: AAF15365.1;
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SEQUENCE 782 AA; 90082 MW; BEIF4CF2883903FD CRC64;
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01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RAB GDP-DISSOCIATION INHIBITOR.
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01-NAY-2000 (TYEMBLEEL. 13, Last sequence update)
01-NAY-2000 (TYEMBLEEL. 13, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN-1.
                                                                                 01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY-ASSOCIATED PROTEIN 1.
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Best Local Similarity 100.
Matches 8; Conservative
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202 LTPLEELY 209
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202 LIPLEELY 209
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Q9U414;
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09970A4
1D 09970A4
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DT 01-NOV
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Mueller W.E.G.;
Aquatler Toxicol. 37:157-168(1997).
EMBL: X94983; CA64439.1; -.
HSSP: P21856; IGND.
InterPro: IPR020055; Rab_GDI_REP.
Pfam: PR00996; GDI: 1.
PRINTS; PR00991; RABGDIREP.
SEQUENCE 448 AA: 50215 MW; 0F94A980DC6BEIA2 CRC64;
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Viruses; dabNA viruses, no RNA stage; Poxviridae; Entomopoxvirus Entomopoxvirus B.
NCBL_TaxID-28321;
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MEDLINE=20396580; PubMed=10936094;
Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W.,
Moyer R.W.;
Complete Genomic Sequence of the Amsacta moorei Entomopoxvirus:
Analysis and Comparison with Other Poxviruses.";
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Bawden A.L., Glassberg K.J., Diggans J., Shaw R., Farmerie W., Moyer R.W.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF250284; AAC02813.1; -.
SEQUENCE 149 AA; 17470 MW; 877185CEA034F840 CRC64;
                                                                                     Geodia cydonium (Sponge).
Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
Astrophorida; Geodiidae; Geodia.
NCBI_TaxID=6047;
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87.8%; Score 36; DB 12; Length 149;
Best Local Similarity 75.0%; Pred. No. 11;
Matches 6; Conservative 2; Mismatches 0; Indels
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01-WAR-2001 (TrEMBLrel. 16, Last sequence update)
01-WAR-2001 (TrEMBLrel. 16, Last annotation update)
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              GDP-DISSOCIATION INHIBITOR
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46 LSPLEELY 53
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85 ITPVEELY 92
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Human Human Human homologue of

Lysine/Serine Peptide #6352

polypeptide

Human Human

Sequence:

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Searched:

Database

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Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum RAP-1 antigenic epitope, P604.
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(USSH ) US DEPT HEALTH & HUMAN SERVICES.
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AAY85565
AAW08983
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AAB75556
AAU01060
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AAM39916
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AAM38657
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AAY70710
AAM42043
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AAU01092
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AAB93940
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AAY32210
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AAM41702
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626
2559
176
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WO200011179-A1.
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Polypeptide antige
Ri paraneoplastic
Arabidopsis thalia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falcipa
                                                                                                      (without alignments)
18.999 Million cell updates/sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                       Search time 66.28 Seconds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Description
                                                                                                                                                                                                                                                                                                                                                                                    **SinssycatarygeneseqyAal980.DAT:**

**Sinssycgdata/geneseqyAal981.DAT:**

**Sinssycgdata/geneseqyAal981.DAT:**

**Sinssycgdata/geneseqyAal981.DAT:**

**Sinssycgdata/geneseqyAal983.DAT:**

**Sinssycgdata/geneseqyAal984.DAT:**

**Sinssycgdata/geneseqyAal984.DAT:**

**Sinssycgdata/geneseqyAal987.DAT:**

**Sinssycgdata/geneseqyAal987.DAT:**

**Sinssycgdata/geneseqyAal987.DAT:**

**Sinssycgdata/geneseqyAal987.DAT:**

**Sinssycgdata/geneseqygeneseqpyAal981.DAT:**

**Sinssycgdata/geneseqygeneseqpyAal981.DAT:**

**Sinssycgdata/geneseqygeneseqpyAal991.DAT:**

**Sinssycgdata/geneseqygeneseqpyAal999.DAT:**

**Sinssycgdata/geneseqygeneseqpyAal999.DAT:**
         a 4.5
Compugen Ltd.
                                                                                                                                                                                                                                                       fotal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                522463 seqs, 74073290 residues
                                                                                        ٠.
            GenCore version
Copyright (c) 1993 - 2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SUMMARIES
                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                      January 29, 2002, 10:21:56

    protein search, using sw model

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AAB98924
AAY54617
AAB98923
AAE01347
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AAR06991
                                                                                                                                                                                          BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                 SSPSSTKSSPSNVKSAS 17
                                                                                                                               US-09-763-397A-22
79
                                                                                                                                                                                                                                                                                  seq length: 0
seq length: 200000000
                                                                                                                                                                                                                                                                                                                                                                         A_Geneseq_1101:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB
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3350
3350
530
328
328
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1141
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86.7
662.7
660.8
660.8
660.8
558.2
58.2
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112...
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220...
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68.5
49
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Perfect score:
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                                                                                                                                                                                                                                                                                  Minimum DB s
Maximum DB s
                                                               protein
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Lal AA, Shi YP, Hasnain SE;

WPI; 2000-237654/20

AAG23324 AAG23323 AAG23322

2 2 4 3 10 10 11

Result No.

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Qy
                                                                                   The present sequence is the antigenic epitope P604, derived from choptry associated protein-1 (RAP-1) of the asexual blood stage of proper protein and protein compared to the construction of recombinant protein CDC/VINIMALVAC-1, which is a multivalent, multistage malarial protein CDC/VINIMALVAC-1, which is a multivalent, multistage malarial protein CDC/VINIMALVAC-1, which is a multivalent, multistage malarial captiope from tetanus toxold and 21 antigenic epitopes from tetanus toxold and 21 antigenic epitopes concircumsporozoite protein (CSP-1), sporozoite surface protein-1 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (SSP-1), MSP-2, apical membrane antigen-1 (AM-1), erythrocyte binding caption-175, rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for
                                                                                                                                                                                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; r-cell epitope; tetanus toxoid; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein:2; SSP-2; liver stage antigen:1; LSA-1; merozoite surface protein:1; MSP-1; MSP-2; appical membrane antigen:1; AMA-1; erythrocyte binding antigen:175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; prevention; anti-CDC/NIIMALVAC-1 antibody;
                                                                                                                                                                                                                                                                                                                                                              Gaps
             Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                23..350
/label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
                                                                                                                                                                                                                                                                                                                                                             .;
0
                                                                                                                                                                                                                                                                                                                                   Length 16;
                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1..22
/label- Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                       DB 21; L 4.5e-05;
                                                                                                                                                                                                                                                                                                                                       94.9%; Score 75; DB 100.0%; Pred. No. 4.5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant vaccine CDC/NIIMALVAC-1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70278 standard; Protein; 350 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Chimeric - Apis sp.
Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                                     Claim 2; Page 17; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99WO-US18869
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0097703
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    06-JUN-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                           Query Match 94.9
Best Local Similarity 100.
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           1 SSPSSTKSSPSNVKSA 16
                                                                                                                                                                                                                                                                                                                                                                                                          WO200011179-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            honey bee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAY70278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Peptide
                                                                                                                                                                                                                                                                                                         Sequence
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant comprises, melittin signal peptide, (His)6 tag, Tr-call epitope from tetanus toxoid and 21 antigenic epitopes from circumsporozoite from tetanus toxoid and 21 antigenic protein-2 (SSP-2), liver stage cortein (CSP), sporozoite surface protein-1 (MSP-1), MB-2, apical contigen-1 (LSA-1), merozoite surface protein-1 (MSP-1), MB-2, apical comborance antigen-1 (MAN-1), erythrocyte binding antigen-175 (BBA-175), Theoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting in falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                    Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Antigenic polypeptide and DNA encoding it - having a determinant cross reactive with those on the rhostry organelles of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 350;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                polypeptide antigenic to rhostry organelles of Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 68.5; DB 21;
Pred. No. 0.012;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
(NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Malaria; vaccine; rhoptry organelles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR06991 standard; protein; 782 AA.
                                                                                                                                                                                                                                                                                                  Claim 3; Page 43-44; 52pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ..
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                90EP-0104561.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           89GB-0005857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 86.7%;
94.4%;
                                                                              Hasnain SE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SSPSSTK-SSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-JAN-1991 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ridley RG, Scaife JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1990-291721/39.
N-PSDB; AAQ06000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 17; Conserv
                                                                                                                                 2000-237654/20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 350 AA;
                                                                                   Shi YP,
                                                                                                                                                         N-PSDB; AAZ51336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-MAR-1990;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-MAR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       26-SEP-1990
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                                                                                   Lal AA,
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FX8X5000XX8

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WO200149850-A1.
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                                                                                                                                                                                                                       Sequence
                                                                                                                                                                            isolated
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Domain
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                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ri8; paraneoplastic opsoclonus; PO; cerebellar; expression vector; library; Ri; paraneoplastic antigenic polypeptide; phagemid; lambda-Ri8; helper phage; R408; anti-R1; antiserum; fusion protein; antibody; dideoxy method; open reading frame; PCR; probe.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Ri para-neoplastic antigenic polypeptide and antibody specific for para-neoplastic antigen - used in the diagnosis and treatment of para-neoplastic opsocionus
                                                                                                                                                                                                                                                                                                        ..
                                                                                                       expression system using plasmid pMC9, and may then be used for immunisation against malaria. The product may also be used diagnostically to detect Abs directed against the parasite.
                                                                                  Gene product may be isolated from a transformed E.coli (Y1088)
                                                                                                                                                                                                                                                        Score 68.5; DB 11; Length 782;
Pred. No. 0.03;
); Mismatches 0; Indels 1
merozoite form of the malaria parasite P falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ri paraneoplastic antigenic polypeptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Posner JB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SLOK ) SLOAN KETTERING INST CANCER.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR28888 standard; Protein; 530 AA.
                                        Claim 1; Fig 2a-b; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        197..232
/note= "HOM #2"
447..482
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                                                                                                                                                                                                                                                        86.7%;
94.4%;
                                                                                                                                                                                                                                                                                                                                                                    92WO-US03249
                                                                                                                                                                                                                                                                                                                                              1 SSPSSTK-SSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     25-MAR-1993 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Darnell RB, Furneaux HM,
                                                                                                                                                                                                                                                        Query Match 86.7
Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1992-398791/48.
N-PSDB; AAQ30802.
                                                                                                                                                                                            782 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         21-APR-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-APR-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      W09219635-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAR28888;
                                                                                                                                                                                              Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Region
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plasmid being designated pRi8 (see also AAQ30801). pRi8 was cloned and propagated in E. coli. pRi8 encoded a protein of mol. wt. 40 kD which is recognised by anti-Ri antiserum. This Ri8 fusion protein was used as an antigen to affinity purify antibody from the anti-Ri antiserum. The DNA sequence of pRi8 was determined by the dideoxy method and an open reading frame encoding approx. 340 antino acids was identified. Regions of this sequence could be used to make PCR probes such that additional clones representing the full length Ri gene could be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New null allele of the Arabidopsis thaliana ABI4 gene, useful for imparting insensitivity to abscisic acid and ability to germinate and grow on saline soils \dot{}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ABI4 gene; transactivator; APETALA2 domain; AP2 domain; chromosome 2;
                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
55..110
/label- APETALA2_domain
/note-"Binds to C-repeat/DRE regulatory elements;
acts as a transactivator"
                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C-repeat/DRE regulatory element; abscisic acid insensitivity; salt tolerance; seed germination; saline soil; abi4 allele.
                                                                                                                                                                                                                                                                           Length 530,
                                                                                                                                                                                                                                                                                                                       3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quesada Perez V, Ponce Molet RM, Micol Molina JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Arabidopsis thaliana abi4 allele-encoded protein.
                                                                                                                                                                                                                                                                           ; DB 13;
: 16;
                                                                                                                                                                                                                                                                                                                         Mismatches
                                                                                                                                                                                                                                                                             Score 49;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (UYEL-) UNIV ELCHE MIGUEL HERNANDEZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAB98924 standard; peptide; 140 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig 5; 26pp; Spanish.
                                                                                                                                                                                                                                                                                                                           4;
                                                                                                                                                                                                                                                                             62.0%;
58.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         03-JAN-2001; 2001WO-ES00003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                03-JAN-2000; 2000ES-0000004
                                                                                                                                                                                                                                                                                                                                                                                        |||:||||||: |
|176 ssptttksspsdpmtts 192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                             Query Match 62.0
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2001-441881/47.
                                                                                                                                                                                                                530 AA;
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1 SSPSSTKSSPSNVKSAS 17

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Db
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This sequence represents the Arabidopsis thaliana Abi4 protein of the invention. ABI4 is involved in regulating seed development, production of seed nutrient reserves and desiccation protectatis. The nucleic acid can be used to create transgenic plants with modified regulation of seed viability, production of nutrient reserves and desiccation protectants in seeds and vegetative stress tolerance, e.g. to drought or salinity, and
                                                                                                                                                                                                                                                        ö
Arabidopsis thallana homozygous for the abi4-2 (san5) allele are tolerant of high concentrations of sodium chloride (150 mM), mannitol (400 mM), potassium chloride (150 mM) and sodium sulphate (75 mM). The abi4-2 (san5) allele is used to produce Arabidopsis plants that are able to germinate and grow in highly saline soils in which wild-type plants connot survive. Orthologous alleles from other crop plants can be used to impart similar properties. The present sequence represents the abi4 protein encoded by the mutant allele abi4. This protein contains the APETALA2 domain, but is C-terminally truncated with respect to the wild-type ABI4 protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Abi4 gene; seed development regulation; seed nutrient reserve production; desiccation protectant; vegetative stress tolerance.
                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Arabidopsis thaliana ABI4 gene, mutants and variants, useful for creating transgenic plants with e.g. modified regulation of seed viability and vegetative stress tolerance
                                                                                                                                                                                                                                                            ;
0
                                                                                                                                                                                                                             Length 140;
                                                                                                                                                                                                                                                            4; Indels
                                                                                                                                                                                                                                 DB 22;
                                                                                                                                                                                                                                                             2; Mismatches
                                                                                                                                                                                                                                    Score 48;
                                                                                                                                                                                                                                                    Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                 AAY54617 standard; Protein; 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis Abi4 protien sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 6; Fig 4; 68pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   98US-0083334.
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                                                                                                                                                                                                                                    60.8%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to abscisic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (REGC ) UNIV CALIFORNIA.
(GEHO ) GEN HOSPITAL CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                             SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2000-013434/01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AA;
                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        27-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     27-APR-1998;
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                                                                                                                                                                                                                                                                     11;
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                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY54617;
                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                       Query Match
Best Local 3
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                                                                                                                                                                                                                                                                     Matches
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The invention relates to a null, or extremely hypomorphic, allele of the invention relates to anull, or extremely hypomorphic, allele of the ABI4 gene of Arabidopsis thaliana that confers insensitivity to the ABI4 germination. The allele, designated sans or abit 4.2, has a deletion of one of the three adenines at cesignated sans or abit 4.2, has a deletion of one of the three adenines at positions 277-279 relative to the wild-type allele (designated ABB4), consisting from amino cid residue 44 onwards. The abit 4-2 protein contain the APETALA2 (AP2) domain located between containing from amino acid residue 44 onwards. The abit 4-2 protein containing from amino acid residue ABB4 protein (AABB9925) which mediates residues 55-110 in the wild-type ABB4 protein (AABB9923) which mediates contained and activity at C-repeat/DRE regulatory elements. Seeds of transactivational activity at C-repeat/DRE regulatory elements. Seeds of this concentrations of sodium chloride (150 mM), mannitol (400 mM), containing the concentrations of sodium sulphate (75 mM). The abit 4.2 potassium chloride (150 mM) and sodium sulphate (75 mM). The abit 4.2 germinate and grow in highly saline soils in which wild-type plants cannot survive. Orthologous alleles from other crop plants can be used to impart similar properties. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New null allele of the Arabidopsis thaliana ABI4 gene, useful for imparting insensitivity to abscisic acid and ability to germinate and grow on saline soils
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                       ABI4 gene; transactivator; APETALA2 domain; AP2 domain; chromosome 2; C-repeat/ORE regulatory element; abscisic acid insensitivity; salt tolerance; seed germination; saline soll; wild-type allele.
                                                                                                                                                                                                                                                                     Location/Qualifiers
55..110
/label= APETALA2_domain
/note= "Binds to C-repeat/DRE regulatory elements;
acts as a transactivator"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .;
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tive 2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Micol Molina JL;
                                                                                                                          Arabidopsis thaliana ABI4 wild-type protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYEL-) UNIV ELCHE MIGUEL HERNANDEZ.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quesada Perez V, Ponce Molet RM,
            AAB98923 standard; peptide; 328 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 5; 26pp; Spanish.
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Best Local Similarity 64.7
Matches 11; Conservative
                                                                                             (first entry)
                                                                                                                                                                                                                                                  Arabidopsis thaliana.
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                                                                                           09-OCT-2001
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                                                         AAB98923;
                                                                                                                                                                                                                                                                                           Key
Domain
AAB98923
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Gaps

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DB 21; Length 328; 4; Indels

Pred. No. 13; 2; Mismatches

Score 48;

60.8%;

Query Match Best Local Similarity 64.7 Matches 11; Conservative

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ò qq AAE01347;

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                   Arabidopsis thaliana protein fragment SEQ ID NO: 26590.
                    AAG23324 standard; Protein; 139 AA.
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990S-0134256.
990S-0134218.
990S-0134219.
990S-0134370.
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99US-0128714.
99US-0129845.
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99US-0130510.
99US-0130891.
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99US-0132048.
99US-0132407.
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99US-0136392.
99US-0136782.
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99US-0127462
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99US-0135629.
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                                                                                                                   (first entry)
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                                                                                                                                                                                                                                                                     termination sequence
                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana
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14-MAY-1999;
14-MAY-1999;
14-MAY-1999;
18-MAY-1999;
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06-APR-1999;
08-APR-1999;
16-APR-1999;
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27-MAY-1999;
28-MAY-1999;
                                                                                                                17-OCT-2000
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05-MAY-1999;
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06-MAY-1999;
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23-APR-1999;
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11-MAY-1999;
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24-MAY-1999;
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                                                                     AAG23324;
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07-JUN-19
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AAG23324
                                                                     PART OF THE PROPERTY OF THE PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for modulating a response in a target plant to abscist acid (ABA) by introducing a DNA construct comprising an ABA-associated sequence operably linked to an early kernel/embryo promoter into the plant. The method also involves modulating ABA perception and signal transduction in developing seeds. The method is used to produce plants, particularly cereal plants such as maize, which have a modified response to ABA so that an increase in yield can be produced. The plants are protected against any harmful/detrimental caffects of stress and adverse environmental conditions. The ABA function is disrupted in a tissue and developmental preferred manner so that female reproductive tissue is insulated from the stress or adverse environmental conditions. Other plants which can be transformed include rice, cotton, citrus trees, tomatces, pines, soybean, peanut and olive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA constructs containing an abscisic acid-associated sequence are used to modulate a response in a plant to abscisic acid so that the plants are protected against any harmful or detrimental effects of stress and environmental conditions -
                                                                                                                                                                                                                                                                                                                                                                                     Abscisic acid; ABA; ABA-insensitive; ABI4; signal transduction;
kernel embryo promoter; cereal plant; maize; rice; cotton; citrus tree;
tomato; pine; soybean; peanut; olive.
                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana ABA (abscisic acid)-insensitive 4, ABI4 protein.
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1ve 2; Mismatches 4; Indels
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                                                                                                                                                                                        AAE01347 standard; Protein; 328 AA.
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                                           |||||| || || :| :||
| sspssvssssssvsaas 129
                                                                                                                                                                                                                                                                                         31-JUL-2001 (first entry)
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                 1 SSPSSTKSSPSNVKSAS 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana
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Matches 11; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence, 328 AA;
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99US-0139458 99US-0139459

18-JUN-1999 18-JUN-1999

Query Match

113

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99US-0139457

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AAG23323;
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99US - 0147302
99US - 0147302
99US - 0147260
99US - 0147416
99US - 0147433
99US - 0147433
99US - 0148171
99US - 0148171
99US - 0148171
99US - 0148171
99US - 0148341
99US - 0148565
99US - 0148565
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99US-0149723.
99US-0149929.
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990S-0145913.
990S-0145918.
990S-0145918.
990S-0145951.
990S-0146386.
990S-0146388.
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990S-0144884
990S-0144884
990S-0145086.
990S-0145085.
990S-0145087.
990S-0145087.
990S-0145087.
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99US-0142055.
99US-0142390.
99US-0142390.
99US-0142320.
99US-0142377.
99US-0142377.
99US-0143624.
99US-0144085.
99US-0144085.
99US-0144085.
99US-0144332.
99US-0144332.
99US-0144333.
99US-0144333.
     99US-0139460.
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PR 27-MG-1999; 9918-0151300.

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Pred. No. 11;
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Human secreted protein; autoimmune disorder; hyperproliferative disorder; cardiovascular disorder; anglogenesis; nervous system disorder; bacterial infection; viral infection; fungal infection; ocular disorder; wound healing; tissue regeneration; epithelial cell proliferation; skin ageing; chemotaxis; IgG Fc region.
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Pred. No. 11;
4; Mismatches
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56.2%;
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99US-0160815
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15-SEP-1999;

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The sequence represents a human secreted protein encoded by a nucleic acid of the invention. Secreted proteins and their related nucleic acids can be used in the diagnosis of or susceptibility to a pathological condition by determining the presence or absence of a mutation in a nucleic acid or the presence or amount of expression of a secreted condition by determining the presence or amount of expression of a secreted condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. The antibodies to the polypeptides can also be used in alleviating symptoms associated with disorders and in diagnostic alleviating symptoms associated with disorders and in diagnostic immunoassays e.g. radioimmunoassays or enzyme linkedoc immunosorbent carbuits, hyperproliferative disorders e.g. neoplasms of the breast or liver, cardiovascular disorders e.g. neoplasms of the breast or disorders e.g. cerebral ischaemia, angiogenesis, nervex, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac arrest, cerebrovascular disorders e.g. cardiac aurest, cerebrovascular disorders e.g. corneal infection. The peptides can also be used to aid wound healing and epithelial cell proliferation, to help prevent skin ageing due to sumburn, to maintain organs before transplantation, to regenerate tissues, in chemotaxis and as a food cransplantation, to regenerate tissues, in chemotaxis and as a food
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                    Nucleic acids encoding 26 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. Gaucher's disease, Alzheimer's disease, Scimitar syndrome, Creutzfeldt-Jacob disease, diabetes mellitus and multiple sclerosis
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Pred. No. 19;
; Mismatches 5; Indels
                                                                                                                                                                     Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 399; 412pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  58.28;
                                                                                                             (HUMA-) HUMAN GENOME SCI INC
26-SEP-2000; 2000WO-US26337.
                                                        99US-0155806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                        Komatsoulis GA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SSPSSTKSSPSNVKSAS 17
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Best Local Similarity
Matches 11; Conserv
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                                                                                                                                                                                                                                                             N-PSDB; AAS02655
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                                                             27-SEP-1999;
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New maize replication protein A useful for genetic transformation, gene targeting in plants and modulating DNA metabolism -
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                                                                                                                                                                                                                                                                  The present sequence is the maize replication protein A (RPA) middle subunit homologue-1 (ZmRPAMSH1). RPA is a single-stranded DNA-binding protein required for multiple processes in DNA metabolism, like DNA replication, repair mechanism (e.g. nucleotide excision and double stranded (ds) DNA break repair) and recombination. The gene for the zmRPAMS homologue is mapped to chromosome 5. This sequence has fungicale, virucide and insecticidal activity. DNA encoding RPA is used for modulating DNA metabolism, influencing cell cycle, enhancing homologous recombination and increasing pathogen resistance in plants. Pests that can be controlled include fungal pathogens, viruses, pests that can be controlled include fungal pathogens, viruses, nematodes and insects. Antisense sequences can be used to block RPA expression and promote non-specific recombination events. RPA protein can be used to improve genetic manipulation and also in gene therappy.
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Pred. No. 22;
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                                                                                                                                                                                                                                             Claim 1c; Page 88; 101pp; English.
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                                                                               (PION-) PIONEER HI-BRED INT INC
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99WO-US21277.
                                98US-0100690.
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190 stptslksspapvtsgs 206
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Best Local Similarity
Matches 10; Conserv
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                                                                                                                                                              N-PSDB; AAZ52287
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11-MAR-1999;
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                                17-SEP-1998;
11-MAR-1999;
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                                                                                                                 Mahajan P;
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The present sequence is the maize replication protein A middle subunit homologue-2 and 3 (ZmRPAMSH2 and ZmRPAMSH3). RPA is a single-stranded DNA-binding protein required for multiple processes in DNA metabolism, like DNA replication, repair mechanism (e.g. nucleotide excision and double stranded (ds) DNA break repair) and recombination. The gene for the ZmRPAMS homologue is mapped to chromosome 5. This sequence has fungicide, virucide and insecticidal activity. DNA encoding RPA is used for modulating DNA metabolism, influencing cell cycle, enhancing homologous recombination and increasing pathogen resistance in plants. Pests that can be controlled include fungal pathogens, viruses, nematodes and insects. Antisense sequences can be used to block RPA expression and promote non-specific recombination events. RPA protein can be used to improve genetic manipulation and also in gene therapy.
                                                                New maize replication protein A useful for genetic transformation, gene targeting in plants and modulating DNA metabolism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New maize replication protein A useful for genetic transformation, gene targeting in plants and modulating DNA metabolism -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Maize; Replication protein A; RPA; middle subunit; ZmRPAMSH; virucide; fungtide; insecticide; chromosome 5; DNA-binding protein; DNA repair; DNA metabolism; DNA replication; cell cycle; homologous recombination; pathogen resistance; fungl; virus; nematode; insect; gene therapy;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 46; DB 21; Length 273;
Pred. No. 22;
); Mismatches 4; Indels
                                                                                                                 Claim 1c; Page 90-91; 101pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAY70707 standard; Protein; 273 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    58.2%;
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190 stptslksspapvtsgs 206
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Best Local Similarity 58.8
Matches 10; Conservative
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            2000-271452/23.
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N-PSDB; AAZ52289.
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                              N-PSDB; AAZ52288
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11-MAR-1999;
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Claim 1c; Page 93; 101pp; English

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Gaps

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            The present sequence is the maize replication protein A (RPA) middle subunit homologue-4 (ZmRPAMSH4). RPA is a single-stranded DNA-binding protein required for multiple processes in DNA metabolism, like DNA replication, repair mechanism (e.g. nucleotide excision and double stranded (ds) DNA break repair) and recombination. The gene for the ZmRPAMS homologue is mapped to chromosome 5. This sequence has fungicide, virucide and insecticidal activity. DNA encoding RPA is used for modulating DNA metabolism, influencing cell cycle, enhancing homologous recombination and increasing pathogen resistance in plants. Pests that can be controlled include fungal pathogens, viruses, nematodes and insects. Antisense sequences can be used to block RPA expression and promote non-specific recombination events. RPA protein can be used to improve genetic manipulation and also in gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                                                                      Length 273;
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Pred. No. 22;
3; Mismatches 4;
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                                                                                                                                                                                                                                                                                                                                                                                                                         58.2%;
58.8%;
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190 stptslksspapvtsgs 206
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Best Local Similarity 58.8
Matches 10; Conservative
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Appli
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APPLICANT: DARNELL, ROBERT B.
APPLICANT: DARNELL, ROBERT B.
APPLICANT: PURNEAUX, HENRY B.
TITLE OF INVENTION: ANTHEN RECOGNIZED BY ANTIBODIES ASSOCIATED
TITLE OF INVENTION: WITH PARANEOPLASTIC OPSOCLONUS AND METHODS OF
TITLE OF INVENTION: USE THEREOF
CORRESPONDENCES: 4
CORRESPONDENCE ADDRESS:
               Sequence Seq
                                                                                                                                                                                                                                                                                                   Sequence
 Sequence
                                                                                                                                                                                                                                                                                                                       Sequence
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Pred. No. 5.3;
                               US-08-478-435-8

US-08-478-435-10

US-08-337-483-10

US-08-337-483-10

US-08-478-373-10

US-08-474-671-10

US-08-474-671-10

US-08-483-577A-10

US-08-897-438-8

US-08-897-438-10

US-08-897-438-10

US-08-897-438-10

US-08-897-438-10

US-08-897-438-10

US-08-897-438-10

US-08-816-346-58

US-08-335-411-58

US-08-335-411-58

US-08-816-346-58
                                                                                                                                                                                                                                                                                                                                                                                ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/187,793
FILING DATE:
CLASSIFICATION NUMBER: US/08/187,793
FILING DATE:
APPLICATION NUMBER: US/09/1559
FILING DATE: 25-APR-1991
ATTORNEY/AGENT INFORMATION:
NAME: WHITE, JOHN P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 39227
TELECOMMUNICATION INFORMATION:
TELECHOME: (212) 977-9550
TELECHAR: (212) 664-0525
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: U.S.A.
2IP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 4, Application US/08187793; Patent No. 5614371; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: COOPER & DUNHAM
30 ROCKEFELLER PLAZA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (212) 664-0525
TELEX: (212) 422523 COOP UI
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    62.0%;
58.8%;
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LENGTH: 530 amino acids
TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ; MOLECULE TYPE: protein US-08-187-793-4
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: NEW YORK
RY: U.S.A.
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Best Local Similarity
ADDRESSEE:
STREET: 30
                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-08-187-793-4
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STATE:
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Sequence 15, Appli
Sequence 4, Appli
Sequence 5, Appli
Sequence 2, Appli
Sequence 148, App
Sequence 2, Appli
Sequence 1, Appli
Sequence 1, Appli
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11.866 Million cell updates/sec
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Patent No. 5260432
Sequence 1, Appli
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Sequence 8,
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Sequence 2,
                                                                                                                             ; Search time 32.24 Seconds
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Sequence 5
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2: /cgn2_6/ptodata/2/laa/5B_COMB.pep:*
3: /cgn2_6/ptodata/2/laa/6A_COMB.pep:*
4: /cgn2_6/ptodata/2/laa/6B_COMB.pep:*
5: /cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/2/laa/pcTuS_COMB.pep:*
                 GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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US-08-886-7514-5
US-08-887-4148
US-08-897-438-148
US-08-185-282-1
US-08-185-282-2
US-08-185-282-3
US-08-185-282-3
US-08-185-282-3
US-08-185-282-3
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US-08-843-993-1
US-09-059-520A-1
US-09-344-275-1
US-08-481-814A-8
US-08-836-582-2
US-09-265-566-2
PCT-US96-03916-15
                                                                                                                                                                                                                                                                                                                                                                        Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-09-300-672-2
US-08-808-599A-41
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US-08-613-009A-19
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                                                                                                                                                                                                                                                                                                                                     212252 seqs, 22503292 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                             January 29, 2002, 10:24:14

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                           1 SSPSSTKSSPSNVKSAS
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                                                                                                                                                                                              US-09-763-397A-22
79
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Maximum DB seq length: 200000000
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Match Length DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Perfect score:
                                                                                                                                                                                                                                                                                Scoring table:
                                                                                          OM protein
                                                                                                                                                                                                                                                                                                                                       Searched:
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FUNAS, RONALD M.:UMESONO, KAZUHIKO
TITLE OF INVENTION: HUMAN GAMMA RETINOIC ACID RECEPTOR DNA
NUMBER OF SEQUENCES: 4
                                                                                                                                                                                                                                                                           ő
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 41; DB 6; Length 143;
Pred. No. 19;
                                                                                                                                                                                                                                   Score 43; DB 3; Length 145;
Pred. No. 9.9;
4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM...
OPERATING SYSTEM...
SOFTWARE: FastSEQ for Windows Version 2.0
SURRENT APPLICATION NUMED. DATA.
APPLICATION NUMBER...
FILING DATE: F11ed Herewith
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
F11LING DATE:
F11LING DATE:
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
TITLE OF INVENTION: 4
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2; Mismatches
REFERENCE/DOCKET NUMBER: P-LA 2256
TELECOMMUNICATION INFORMATION:
TELEFRONE: (619) 535-8949
TELEFRAX: (619) 535-8949
INFORMATION FOR SEO ID NO: 41:
SEQUENCE CHARACTERISTICS:
LENGTH: 145 anino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/370,407
FILING DATE: 22-JUN-1989
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 5
US-08-843-993-1
Sequence 1, Application US/08843993
Sequence 1, Spaint No. 5739010
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZUP: 94304
COMPUTER, READABLE FORM:
MEDIUU TYPE: Diskette
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51.9%;
72.7%;
                                                                                                                                                                                                                                                54.4%;
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Best Local Similarity 72.7
Matches 8; Conservative
                                                                                                                                                                                                                                                Query Match
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                          3 PSSTKSSPSNVKSAS 17
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| 129 SSPSSNRSSPA 139
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;Patent No. 5260432
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US-08-808-599A-41
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; Sequence 41, Application US/08808599A
; Patent No. 6111099:
GENERAL INFORMATION:
TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
TITLE OF INVENTION: Proteins and Methods to Inhibit Implantation
STREET: 4370 La Jolla Village Drive, Suite 700
STREET: California
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
                                                                                                                                                                                                                                 GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: FINESISTEIN, Ruth R.
APPLICANT: Goodman, Howard M.
APPLICANT: Goodman, Howard M.
APPLICANT: Goodman, Howard M.
APPLICANT: Wang, Ming-Tal
TILLE OF INVENTION: QUALITY AND COLD-TOLERANCE
FILE REFERENCE: 480:89(HV)
CURRENT FILLING DATE: 1999-04-27
NUMBER OF SEQ ID NOS: 16
                             Gaps
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                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATEMENT Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/808,599A
FILING DATE: 28 FEBS-1997
                               3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pred. No. 4.4;
; Mismatches
                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/317,522
FILING DATE: 04-0CT-1994
PRIOR APPLICATION NUMBER: US 08/439,818
APPLICATION NUMBER: US 08/439,818
FILING DATE: 12-MAY-1995
ATTORNEY/AGENT INFORMATION:
NAME: Campbell, Cathryn A.
REGIŞTRATION NUMBER: 31,815
                                                                                                                                                                                                              Sequence 2, Application US/09300672 Patent No. 6248937
                                        4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match 60.8%;
Best Local Similarity 64.7%;
Matches 11; Conservative
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176 SSPTTTKSSPSDPMTTS 192
                                                                          1 SSPSSTKSSPSNVKSAS 17
                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM: Arabidopsis
US-09-300-672-2
                                          10;
                                                                                                                                                                                                 US-09-300-672-2
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                                          Matches
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Patent No. 5869040
GENERAL INFORMATION:
APPLICANT: Hsu, Yen-Ming
TITLE OF INVENTON: GENE THERAPY METHODS AND COMPOSITIONS
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40; DB 3; Length 345;
Pred. No. 75;
3; Mismatches 5; Indels
     50.6%; Score 40; DB 3; Length 345;
52.9%; Pred. No. 75;
tive 3; Mismatches 5; Indels
                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hillman, Jennifer L.
APPLICANT: Shah, Purvi
TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURREMY APPLICATION DATA:
APPLICATION NUMBER: US/09/334,275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/059,520
FILING DATE:
                                                                                                                                                                                                                 Sequence 1, Application US/09334275 Patent No. 6037132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/COCKET NUMBER: PF-0.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 345 amino acids TYPE: amino acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 50.6%;
Best Local Similarity 52.9%;
Matches 9; Conservative
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                                                                                                      1|| | :|||:| | 70 SSPPSAGNSPSSLKFPS 86
                                                                                1 SSPSSTKSSPSNVKSAS 17
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                                           9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           : SYN00AT01
727885
     Query Match
Best Local Similarity
Matches 9; Conserva
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STATE: CA
COUNTRY:
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                                                                                                                                                                                           US-09-334-275-1
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Pred. No. 75;
3; Mismatches 5; Indels
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Patent No. 6001971

GENERAL INFORMATION:
APPLICANT: Shah, Purvi,
TITLE OF INVENTION: HUMAN TRANSCRIPTION FACTOR
NUMBER OF SEQUENCES: 4
CORRESPONDECE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER REGISELE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/059,520A
FILING DATE: Filed Herewith
PRIOR APPLICATION NUMBER:
                                           PF-0274 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PF-0274 US
NAME: B111ings, Lucy J.
REGISTRATION NUMBER: 36,749
REFRENCE/DOCKET NUMBER: PF-02
TELECOMMUNICATION INPORMATION:
TELEFAN: 415-85-0555
TELEFAX: 415-845-4166
INFORMATION FOR SEO ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                               50.6%;
52.9%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                   LENGTH: 345 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 345 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Similarity 52.9
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                        1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                             70 SSPPSAGNSPSSLKFPS 86
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: single
                                                                                                                                                                                                                            ; IMMEDIATE SOURCE:
; LIBRARY: SYNOOAT01
; CLONE: 727885
US-08-843-993-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LIBRARY: SYNOOATO1
CLONE: 727885
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94304
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STATE: VITIGHIA
COMPUTEY: US
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
COMPUTER: PATENTIN RCLEASE #1.0, Version #1.25 (EPO)
OPERATING SYSTEM: VS/09/265,566
FILING DATE: 10-MAT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 413;
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                                                                                                                                                                                                                                                      DB 3; Length 413;
92;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Nixon & Vanderhye
STREET: 1100 No. 6303335th Glebe Road, 8th Floor
CITY: Arlington
                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Bernards, Rene
APPLICANT: Beijersbergen, Roderick L
TITLE OF INVENTION: Transcription factor E2F-4
CORRESPONDENCE: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5;
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Pred. No. 92;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/836,582
FILING DATE: <URNOWN-
PILING DATE: <URNOWN-
PILING DATE: 15-007-1994
ATTORNEY/AGENT INFORMATION:

NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 620-18
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                              2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-265-566-2
                                                                                                                                                                                                                                                      Score 40;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: <Unknown>
15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 2, Application US/09265566 Patent No. 6303335 GENERAL INFORMATION:
              NAME: Arthur R. Crawford
REGISTRATION NUMBER: 25,327
REFERENCE/DOCKET NUMBER: 62(
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   50.6%;
                                                                                                                                                                                                                                                          50.6%;
58.8%;
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 SSPSSTKSSPSNVKSAS 17
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Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                               309 SSSSSSSSSSNSNSSS 325
                                                                                                                  LENGTH: 413 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                      1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                          Query Match 50.6
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-836-582-2
                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 10
US-09-265-566-2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Version #1.25 (EPO)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSE: Nixon & Vanderhye
STREET: 1100 No. 604599th Glebe Road, 8th Floor
CITY: Arlington
STATE: Virginia
COUNTRY: US
ZIP: 22201-4714
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTE: IBM PC COMPatible
COMPUTE: IBM PC COMPatible
COMPUTE: OF COMPATIBLE
COMPUTE: OF COMPATIBLE
COMPATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                             COMPUTER READBLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/481,814A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application US/08836582
Patent NO. 6045999
GENERAL INFORMATION:
APPLICANT: Bernards. Rene
APPLICANT: Beljersbergen, Roderick L
APPLICANT: APPLICANTION: Transcription factor E2F-4
CORRESPONDENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: Nixon & Vanderhye
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 40;
Pred. No. 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB95/00868
FILING DATE: 18-APPL-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 9423049.7
FILING DATE: 15-NOV-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PATCHIN RELEASE #1.0, CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/836,582 FILING DATE: 14-MAY-1997
                                                                       STATE: Massachusetts
COUNTRY: United States of America
ZIP: 02142
                                                                                                                                                                                                                                                                                                            ATTORNEY AGENT INFORMATION:
NAME: KAPLAIN, WATTEN A
REFERENCE/DOCKET NUMBER: A001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-679-2030
TELEFAX: 617-679-2038
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
                                   14 Cambridge Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                309 SSSSSSSSSNSNSSS 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 413 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                  Biogen, Inc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: Illucar
MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                CLASSIFICATION: 424
                         STREET: 14 CTTY: Cambridge
                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ANTI-SENSE:
US-08-481-814A-8
                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT 9
US-08-836-582-2
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APPLICANT: Yoo, Tai-June
APPLICANT: Yoo, Tai-June
APPLICANT: Cheng, Kuang-Chuan
TITLE OF INVENTION: Diagnostic Assay
NUMBER OF SEQUENCES: 6
CORRESPONDENCE & Askew
ADDRESSEE: Jones & Askew
STREET: 191 Peachtree Street, 37th Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      49.4%; Score 39; DB 1; Length 147; 53.8%; Pred. No. 40;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURREWY APPLICATION DATA:
APPLICATION NUMBER: US/08/276,151
FILING DATE: 14-JUL-1994
CLASSIF LCATION NUMBER: 05.70
ATTORNEY/AGENT INFORMATION:
NAME: TOTCHIA, Ph.D., Timothy E
REGISTRATION NUMBER: 36,700
REFERENCE/DOCKET NUMBER: 36,700
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 843-5481
TELEPHONE: (415) 843-5481
TELEPHONE: (415) 857-0663
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 147 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER REDDABLE FORM:
MDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CARRENT APPLICATION NATA:
APPLICATION NUMBER: US/08/886,751A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/08886751A Patent No. 5885783
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CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Young, Leona 37,266
REGISTRATION NUMBER: 37,266
REFERENCE/DOCKET NUMBER: 2549
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (404) 818-3700
TELEFAX: (404) 818-3799
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 217 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           53.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: Inear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 49.4
Best Local Similarity 53.8
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 SSPSSTKSSPSNV 13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.A.
ZIP: 30303
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US-08-886-751A-5
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                                                                               RESULT 11
PCT-US96-03916-15
Sequence 15, Application PC/TUS9603916
Sequence 15, Application PC/TUS9603916
GENERAL INFORMATION:
APPLICANT: Wild, Martha A.
APPLICANT: Cochran, Mark D.
TITLE OF INVENTION: RECOMBINANT INFECTIOUS LARYNGOTRACHEITIS VIRUS
TITLE OF INVENTION: AD USES THEREOF
NUMBER OF SEQUENCES: 72
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Patent No. 5597719
GENERAL INFORMATION:
APPLICANT: Freed, Ellen
APPLICANT: Ruggieri, Rosamaria
TITLE OF INVENTION: Interaction of raf-1 and 14-3-3 Proteins
NUMBER OF SEQUENCE: 9
CORRESPONDENCE ADDRESS:
ADDRESSE: Cooley Godward et al.
STREET: Five Palo Alto Square
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 5; Length 126;
Pred. No. 34;
1; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: NET ALLES COUNTRY: NET ALLES COUNTRY: NEADABLE FORM:

MEDIUM TYPE: Floppy disk COMPUTER: ENAPPY disk COMPUTER: ENAPPY disk COMPUTER: ENAPPE FLORENS: DEC DOSYMS-DOS SOFTWARE: PATENTIN Release #1.25 CURRENT APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION DATA: APPLICATION NUMBER: US 08/126,597 FILING DATE: 24-SEP-1993 ATTONEY ACENT INDERER: 28,678 REGISTRATION NUMBER: 28,678 REFERENCE/DOCKET NUMBER: 39116-A TELECOMMUNICATION INFORMATION: TELECOMMUNICATION INFORMATION: TELECOMMUNICATION POR SEQ ID NO: 15:
                                                                                                                                                                                                                                                                                                         ADDRESSEE: Cooper & Dunham LLP
STREET: 1185 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
                  309 SSSSSSSSSSNSNSSS 325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 49.4
Best Local Similarity 61.5
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; MOLECULE TYPE: protein
PCT-US96-03916-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94036
COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          USA
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COUNTRY: US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 12
US-08-276-151-4
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APPLICANT: LOOSMOTE, Sheena
APPLICANT: Harkness, Robin
APPLICANT: Ghory Pele
APPLICANT: Chong, Pele
APPLICANT: Cray-Owen, Scott
APPLICANT: Yang, Yan-Ping
APPLICANT: Murdin, Andrew
APPLICANT: Kiein, Michel
TTTLE OF INVENTION: Transferrin Receptor Genes
NUMBER OF SEQUENCES: 160
CORRESPONDENCE ADDRESS:
Annewscere.
                                                                                                                                                                                                                                                                          5: Sim & McBurney
Suite 701, 330 Unviersity Avenue
    Sequence 148, Application US/08483577A Patent No. 6015688 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 647 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     49.4
Query Match
Best Local Similarity 62.5
Matches 10; Conservative
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                                                                                                                                                                                                                                                                                                                                 STATE: Ontario
COUNTRY: Canada
ZIP: MSG 1R7
COMPUTER READABLE FORM:
MEDIUM IYPE: Floppy di
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           linear
                                                                                                                                                                                                                                                                                                   STREET: Suite CITY: Toronto STATE: Ontario COUNTRY: Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
US-08-483-577A-148
  US-08-483-577A-148
                                                                                                                                                                                                                                                                              ADDRESSEE:
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0
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Patent No. 5955270
GENERAL INFORMATION:
APPLICANT: Radford, Alan
APPLICANT: Parish, John H.
TITLE OF INVENTION: EXPLOITATION OF THE CELLULASE COMPLEX OF
TITLE OF INVENTION: NEUROSPORA
NUMBER OF SEQUENCE: 7
CORRESPONDENCE ADDRESS:
ADDRESSE: David A. Jackson, Esq.
                                                                                                                                                                                                                                                        0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 516;
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                                                                                                                                                                                                                Score 39; DB 2; Length 217;
Pred. No. 62;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: David A. Jackson, Esg.
STREET: 411 Hackensack Ave, Continental Plaza, 4th
STREET: Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY disk
MEDIUM TYPE: FLOPPY disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION NUMBER: US/08/676,166A
FILING DATE: 15-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REGISTRATION NUMBER: 26,742
RECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 39; DB 2;
Pred. No. 1.7e+02;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 516 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity 41.2%;
Matches 7; Conservative
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459 ASPISSTAKPSSISTAS 475
                                                                                                                                                                                                                          Query Match
Best Local Similarity 53.8%;
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           , MOLECULE TYPE: protein US-08-676-166A-2
                                                                                        ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: HOMO Sapiens
US-08-886-751A-5
                                MOLECULE TYPE: peptide HYPOTHETICAL: NO ANT.
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET: FLOOR
STREET: Hackensack
STATE: New Jersey
                                                                                                                                                                                                                                                                                                                           :|||: |||: |
127 ASPSALSSSPNNL 139
                                                                                                                                                                                                                                                                                                     1 SSPSSTKSSPSNV 13
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                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 14
US-08-676-166A-2
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Pred. No. 2.2e+02;
1; Mismatches 5; Indels
SOFTWARE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,577A
FILING DATE: 07-JUN-1995
FILING DATE: 07-JUN-1995
FILING PAPLICATION NUMBER: US/08/337,483
APPLICATION NUMBER: US/08/337,483
FRICK APPLICATION NUMBER: US/08/175,116
FRICK APPLICATION NUMBER: US/08/175,116
FRICK APPLICATION NUMBER: US/08/175,116
FRICK APPLICATION NUMBER: US/08/175,116
APPLICATION NUMBER: US/08/175,116
FRILNG APPLICATION NUMBER: US/08/148,968
FRILNG DATE: 08-NOV-1993
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Search completed: January 29, 2002, 10:59:57
Job time: 2143 sec
                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Stewart, Michael I
REGISTRATION NUMBER: 24,973
REFERENCE/DOCKET NUMBER: 1038-511
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (416) 595-1155
TELEFAX: (416) 595-1163
INFORMATION FOR SEQ ID NO: 148:
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GenCore version 4.5
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OM protein - protein search, using sw model

January 29, 2002, 10:26:50; Search time 34.94 Seconds Run on:

(without alignments) 37.063 Million cell updates/sec

US-09-763-397A-22 79 1 SSPSSTKSSPSNVKSAS 17

Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Description	rhoptry-associated	onconeural ventral	hypothetical prote	a-agglutinin core	immediate-early pr	hypothetical prote	regulatory protein	hypothetical prote	hypothetical prote	hypothetical serin	brain and muscle A	Arnt-like PAS prot	probable guanine n	myb-related transc	hypothetical prote	probable MYB47 tra	nitrate assimilati	hypothetical prote	hypothetical prote	protein T26F17.14	hypothetical serin	T-cell activation	protochlorophyllid	hypothetical prote	retinoic acid rece	hypothetical prote	o)	hypothetical prote	hypothetical prote
ID	S27833	I38489	G84826	A41258	A45344	E82537	A25048	T12458	D96507	T41394	JC5405	JE0270	T09144	T51657	T04764	н86320	A41697	T24868	E96624	D86352	T39598	G01037	S04783	E86185	B56558	D84681	T06728	T52384	F71418
80	7	7	7	~	~	7	7	7	~	~	7	~	7	7	7	7	7	7	7	~	~	~	~	7	~	~	~	~	7
Length DB	782	510	328	725	1446	497	515	244	211	349	626	626	2559	214	229	267	892	928	1194	230	230	327	388	402	448	541	542	701	696
% Query Match	86.7	62.0	Ö			59.5	59.5	58.2	57.0	57.0	57.0	57.0	57.0	55.7	55.7	55.7	55.7	55.7	55.7	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4	54.4
Score	68.5	49	48	48	48	47	47	46	45	45	45	45	45		44	44	44	44	44	43	43	43	43	43	43	43	43	43	43
Result No.	-	7	m	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	25	56	27	28	59

30 43 54.4 1032 2 T34433 32 43 54.4 1737 2 A59235 33 442.5 53.4 1807 2 S03124 34 42.5 53.2 317 2 T34434 35 42 53.2 317 2 T39869 36 42 53.2 317 2 T39869 37 42 53.2 453 2 150674 42 53.2 459 2 A41977 44 42 53.2 507 2 S64507 44 42 53.2 507 2 T49913 44 42 53.2 779 2 T49913 45 42 53.2 779 2 T49913		hypothetical prote	unconventional myo	vitellogenin A2 pr	hypothetical prote	immediate-early pr	probable lysophosp	probable leucine-r	retinoic acid rece	retinoic acid rece	retinoic acid rece	hypothetical prote	probable membrane	probable membrane	serine-rich protei	related to BCS1 pr	hypothetical prote
4 4 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		T34433	A59235	S03124	T34434	EDBEIF	T39869	T01281	150674	A41977	A56558	T01564	S63257	S64507	T39903	T49717	T21460
4 4 4 4 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8 8		~	ď	~	N	-	7	7	~	7	7	N	~	7	7	7	7
		1032	1737	1807	2232	1460	317	380	453	459	464	496	503	207	534	779	196
333 333 333 333 334 336 336 425 425 447 447 447 447 447 447 447 447 447 44		54.4	54.4	54.4	54.4	53.8	53.2	53.2	53.2	53.2	53.2	53.2	53.2	53.2	53.2	53.2	53.2
0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0 0		43	43	43	43	42.5	42	42	42	42	42	42	42	42	42	42	42
	ć	30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

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Thopty-associated protein 1 precursor - malaria parasite (Plasmodlum falciparum)

Nalternate names: protective antigen
C; Alternate names: protective antigen
C; Bate: 17-Apr-193 #sequence_revision 17-Apr-1993 #text_change 09-Jun-2000
C; Date: 17-Apr-1993 #sequence_revision 17-Apr-1993 #text_change 09-Jun-2000
A; Title: Characterisation and sequence of a protective rhoptry antigen from Plasmodlu A; Reference number: A45514; MUID: 90348711
A; Accession: A45514
A; Caracterianinary
A; Molecule type: DNA
A; Residues: 1-782 CRI2>
A; Cross-references: GB: M32853; NID: 9160656; PID: 9160657
C; Superfamily: Plasmodlum falciparum rhoptry-associated protein 1
RESULT
```

Gaps 1; Length 782; Indels .; Score 68.5; DB 2; Pred. No. 0.014; 0; Mismatches 0; 86.78; Query Match 86.7 Best Local Similarity 94.4 Matches 17; Conservative

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145 SSPSSTKSSSPSNVKSAS 162 1 SSPSSTK-SSPSNVKSAS 17 ò Db

onconeural ventral antigen-1 - human
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Species: Homo sapiens (man)
C;Accession: 134489
R;Buckanovich, R.J.; Posner, J.B.; Darnell, R.B.
Neuron 11, 657-672, 1993
N*Title: Nova, the Paraneoplastic Ri Antigen, is Homologous to an RNA-Binding Protein A;Reference number: 138489
A;Reference number: 138489
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-510 <RES>
A;Conserieferences: EMBL:U04840; NID:9440877; PIDN:AAA16022.1; PID:9440878
C;Genetics:
A;Genetics:
A;Genetics:

Gaps ; 0 Score 49; DB 2; Length 510; Pred. No. 7.3; 4; Mismatches 3; Indels 4; 62.0%; 58.8%; Query Match 62.0 Best Local Similarity 58.8 Matches 10; Conservative

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1 SSPSSTKSSPSNVKSAS 17

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A; Accession: E8237
A; Status: preliminary
A; Molecule type: DNA
A; Status: preliminary
A; Molecule type: DNA
A; Residues: 1.497 cSIM>A; Casarete cences: GB: AED04067; GB: AED03849; NID: 99107818; PIDN: AAF85399.1; GSPDB: GN
A; Residues: 1.497 cSIM>A; Casarete cences: GB: AED04067; GB: AED03849; NID: 99107818; PIDN: AAF85399.1; GSPDB: GN
A; Experimental source: strain 9a5c st
                                                                                                                                 immediate-early protein - suid herpesvirus 1 (strain Kaplan)
immediate-early protein - suid herpesvirus 1
C:Species: suid herpesvirus 1
C:Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
C;Accession: A45344
R:Vicek. C:; Kozmik, Z.; Paces, V; Schirm, S.; Schwyzer, M.
R:Vicek. C:; Kozmik, Z.; Paces, V; Schirm, S.; Schwyzer, M.
A;Title: Pseudorables virus immediate-early gene overlaps with an oppositely oriented A;Title: Pseudorables virus immediate-early gene overlaps with an oppositely oriented A;Tetrescence number: A45344; MUID:91021039
A;Tetrescession: A45344; MUID:91021039
A;Catus: translation not shown
A;Molecule type: DNA
A;Catus: L1446 CVLC>
A;Cross-references: GB:MA4651; NID:9334070; PIDN:AAA47470.1; PID:9334071
C;Superfamily: herpesvirus immediate-early protein; transcription regulation
C;Keywords: DNA binding: early protein; transcription regulation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hypothetical protein XF2602 (imported) - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C;Accession: E82537
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
R;anonymous, The Aylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A;Attle: The genome sequence of the plant pathogen Xylella fastidiosa.
A;Reference number: A82515; MUID:20365717
A;Reference number A59328 below
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ;;
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ed. No. 14;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 48; DB 1
Pred. No. 29;
2; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 47;
Pred. No. 1
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64.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                60.8%;
Local Similarity 64.7%;
hes 11; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HILLIHIH | |:|
842 SSPASTKSSSSTKSSSS 858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 SSPSSTKSSPSNVKSAS 17
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157 ASPSSTRQVPSNVE 170
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191 ISPSSTSTSPSSTSTSS
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Best Local Similarity
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a-agglutinin core protein AGA1 - yeast (Saccharomyces cerevisiae)
A5 angglutinin attachment protein AGA1; protein N3431; protein YNR044w
N; Alternate names: a-agglutinin attachment protein AGA1; protein N3431; protein YNR044w
C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Species: Saccharomyces cerevisiae
C; Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 29-Oct-1999
C; Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 29-Oct-1999
C; Accession: A1258 #sequence_revision 03-Apr-1992 #text_change 29-Oct-1999
A; Title: The AGA1 product is involved in cell surface attachment of the Saccharomyces C6
A; Reference number: A41258; MID:91304412
A; Residues: 1-725 GROY
A; Residues: 1-725 GROY
A; Residues: 1-725 GROY
A; Reference number: S63346
A; Residues: 1-725 GROY
A; Cross-references: EMBL:271659; NID:91302551; PIDN:CAA96325.1; PID:e239834; PID:9130255
A; Recession: S630-104
A; Experimental source: strain S288C
C; Genetics:
A; Experimental Source: strain S288C
A; Gross-references: EMBL:2715 GROY
A; Gross-references: EMBL:271659; MID:91302551; PIDN:2715 GROY
A; Groys-references: EMBL:271659; MID:91302551; PIDN:2715
                                                                                                                                                                                                                                                                                                                                                                                               Rilin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Roo, H.; Woffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J. Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487
A;Accession: G84826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
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                                                                                                                                                                                                                                                 hypochetical protein At2940220 [imported] - Arabidopsis thaliana ('Species: Arabidopsis thaliana (mouse-ear cress) ('Species: Arabidopsis thaliana (mouse-ear cress) ('Date: 02-Reb-2001 #sequence_revision 02-Reb-2001 #text_change 02-Feb-2001 ('Accession: 694826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 328;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 14R
C;Keywords: qiyooprotein; transmembrane protein
F;8-24/Domain: transmembrane #status predicted <TMI>F;708-724/Domain: transmembrane #status predicted <TM2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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15;
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Pred. No. 6.6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene: SGD:AGA1
A;Cross-references: SGD:S0005327; MIPS:YNR044w
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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Pred. No. 1
5; Mismatch
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52.9%;
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64.7%;
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                                                 11; Conservative
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Best Local Similarity
Matches 9; Conserv
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Best Local Similarity
Matches 11; Conserv
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A; Molecule type: DNA
A; Residues: 1-328 <STO>
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hypothetical protein T12c22.10 (imported) - Arabidopsis thallana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Accession: D96507
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Liu, X.; Liu, Z.A.; Luros, J.S.; Malti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo A;Reference and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Hypothetical serine-rich protein - fission yeast (Schizosaccharomyces pombe)
C;Species: Schizosaccharomyces pombe
C;Species: T41394
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
R;Wood, V.; Rajandream, M.A.; Barrell, B.G.; Murphy, L.; Harris, D.
A;Rocession: T41394
A;Rocession: T41394
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Rocession: T41394
A;Residues: 1-349 
A;Residues: 1-349 
A;Residues: 1-349 
A;Cross-references: EMBL:AL023704; PIDN:CAA19262.1; GSPDB:GN00068; SPDB:SPCC553.10
A;Experimental source: strain 972h-; cosmid c553
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                                                                                                                                                                                                            Gaps
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                                                                                                                                                    Length 244;
                                                                                                                                                                                                         5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     4; Indels
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A:Experimental source: fetal brain; clone DKF2p56400823
C;Genetics:
A;Note: DKF2p56400823.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
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Pred. No. 20;
3; Mismatches
                                                                                                                                                    DB 2
9.8;
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Pred. No. 12;
3; Mismatches
                                                                                                                                                                                                            1; Mismatches
                                                                                                                                                    Score 46;
Pred. No.
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64.7%;
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58.8%;
                                                                                                                                                 Query Match 58.2%;
Best Local Similarity 64.7%;
Matches 11; Conservative
                                                                                                                                                                                                                                                                                                156 SSPSSLSTSPPEVFSAS 172
                                                                                                                                                                                                                                                                  1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 SSPSSTKSSPSNVKSAS 17
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A;Gene: SPDB:SPCC553.10
A;Map position: 3
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Best Local Similarity
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A; Residues: 1-211 <STO>
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A; Map position: 1
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                                                                                                       regulatory protein STE7 - yeast (Saccharomyces cerevisiae)
N:Alternate names: protein D1525; protein YDL159w
C:Species: Saccharomyces cerevisiae
C:Species: Saccharomyces cerevisiae
C:Date: 30-Jun-1988 #sequence_revision 30-Jun-1988 #text_change 24-Sep-1999
C:Accession: A25048; S61054; S67711; S67707
R:Teague, M.A.; Chaleff, D.T.; Errede, B.
Proc. Natl. Acad. Sci. U.S.A. 83, 7371-7375, 1986
A:Title: Nuclectide sequence of the yeast regulatory gene STE7 predicts a protein homolc A:Reference number: A25048; MUID:87016949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; restructs: 1-515 CPONY
A; Restructs: 1-515 CPONY
A; Cross-references: EMBL: Z74207; NID: g1431250; PIDN: CAA98732.1; PID: e253067; PID: g143125
A; Experimental source: strain S288C
A; Experimental source: strain S288C
B; Perea, J.; Blugeon, C.; Delaveau, T.; Jacq, C.
submitted to the Protein Sequence Database, July 1996
A; Reference number: S67693
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A;Residues: 1-515 <POH>
A;Cross-references: EMBL:Z67750; NID:g1061256; PIDN:CAA91587.1; PID:g1061280
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C;Date: 23-Jul-1999 #sequence_revision 23-Jul-1999 #text_change 23-Jul-1999
C;Accession: T12458
                                                                                                                                                                                                                                                                                                                                                                                                          A;Molecule type: DNA
A;Residues: 1-515 <TEA>
A;Cross-references: EMBL:M14097; NID:g172761; PIDN:AAA35118.1; PID:g172762
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 515;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      submitted to the Protein Sequence Database, July 1996 A; Reference number: S67708 A; Accession: S67711
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Pred. No. 15;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        submitted to the EMBL Data Library, November 1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: SGD:S0002318; MIPS:YDL159w
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A;Residudes: 71-515 cpER>
A;Cross-references: EMBL:Z74207; MIPS:YDL159w
A;Experimental source: strain S288C
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A; Accession: $61054
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Best Local Similarity
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A;Molecule type: mRNA
A;Residues: 1-244 <WAM>
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                                                              RESULT
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A; Molecule type: mRNA
A;Residues: 1-676,'L',678-837,'L',839-889,'S',891-1243,'D',1245-1358,'E',1360-1368,'R
A;Cross-references: EMBL:AF032870; NID:92760367; PIDN:AAC38820.1; PID:92760368
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: mediates actin rearrangements required for cell shape changes during g Cs. Superfamily: protein kinase C zinc-binding repeat homology C; Keywords: signal transduction; embryo; GIP exchange F;1151-1200/Domain: protein kinase C zinc-binding repeat homology <KZN>
                                                                                     A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Nolecule type: mRNA
A:Residues: 1-2559 <HRB>
A:Residues: 1-2559 <HRB>
A:Residues: 1-2559 <HRB>
A:Cross-references: EMBL:APO31930; NID:92687355; PID:92687356
B:Barrett, K.; Leptin, M.; Settleman, J.
Cell 91, 905-915, 1997
A:Fliete: The Rho GrPase and a putative RhoGEF mediate a signaling pathway for the CAPARESION: 109223
A:Accession: 109223
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Pred. No. 1.4e+02;
1; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
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A;Cross-references: FlyBase:FBgn0023172
A;Map position: 2; 55F1-2
A;Note: orchestrates cell shape changes during gastrulation
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                                                                                                                                                                                                                                                                                                                                                                                    A; Status: preliminary; translated from GB/EMBL/DDBJ
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Pred. No. 17;
4; Mismatches
R.Haecker, U.; Perrimon, N.
submitted to the EMBL Data Library, October 1997
Reference number: 216586
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ilarity 69.2%;
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C, Keywords: transcription factor
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Matches 9; Conserv
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Matches 9; Conserv
                                                                                  A; Accession: T09144
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JE0270
Arnt-like PAS protein, Arnt3 - mouse
C.Species: Mus musculus (house mouse)
C.Species: Mus musculus (house mouse)
C.Date: 05-Feb-1999 #text_change 21-Jul-2000
C.Accession: JE0270
E.Accession: JE0270
B.Takahata, S.; Sogawa, K.; Kobayashi, A.; Ema, M.; Mimura, J.; Ozaki, N.; Fujii-Kuriyam
B.Ochem. Biophys. Res. Commun. 248, 789-794, 1998
A.Pitile: Transcroptioally active heterodimer formation of an Arnt-like PAS protein, Arnt3
A.Reference number: JE0270; MUID: 98369629
A.Accession: JE0270
A.Molecule type: mRNA
A.Residues: 1-626 <TAK>
A.Residues: 1-626 <TAK>
A.Cross-references: DDBJ:AB014494; NID: 93402482; PIDN: BAA32208.1; PID: 93402483
                                                                                                                                                                          RESULT 11
JOSAGO
DISAGO
DISAGO
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SPECIES: Homo saplens (man)
C;Species: Homo saplens (man)
C;Decies: Homo saplens (man)
C;Accession: JOSAGO; JOSAGO
R;Reda, M.; Nomura, M.
R;Reda, M.; Nomura, M.
Blochem: Blochys. Res. Commun. 233, 258-264, 1997
A;Ittle: CDNA cloning and tissue-specific expression of a novel basic helix-loop-helix/F
                                                                                                                                                                                                                                                                                                                                                                                 site usage.

A;Reference number: JC5404; MUID:97289529
A;Reference number: JC5404; MUID:97289529
A;Accession: JC5405
A;Status: nucleic acid sequence not shown
A;Melecule type: mRMA
A;Residues: 1.626 < IKE>
A;Accession: JC5406
A;Residues: 1.626 < IKE>
A;Accession: JC5404
A;Accession: JC5404
A;Accession: JC5404
A;Accession: JC5404
A;Accession: JC5404
A;Actus: nucleic acid sequence not shown
A;Accession: JC5404
A;Acc
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Pred. No. 35;
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Best Local Similarity 66.7
Matches 10; Conservative
                              1 SSPSSTKSSPSNVKSAS 17
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C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 13-Aug-1999
C;Accession: T04764
R;Bevan. M.;De Haan, M.; Maarse, A.C.; Grivell, L.A.; Bancroft, I.; Mewes, H.W.; Mayer, submitted to the Protein Sequence Database, June 1998
A;Reference number: 215383
A;Reference number: 21538
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Search completed: January 29, 2002, 11:00:39 Job time: 2029 sec

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homo sapien saccharomyc saccharomyc homo sapien saccharomyc saccharomyc saccharomyc caenorhabdi

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saccharomyc saccharomyc caenorhabdi saccharomyc

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KLF3_HUMAN
YP11_YEAST
COQ2_YEAST
MID2_YEAST
E2F4_HUMAN
MAC1_YEAST
SYR_CABEL
YCR6_YEAST
YRC_XEAST
VRG_XEAST
YRC_CABEL
SYR_CABEL
YRC_CABEL
SYR_CABEL
 345
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 Search time 20.36 Seconds (without alignments) 30.614 Million cell updates/sec
      GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                           January 29, 2002, 11:13:51
                               OM protein - protein search, using sw model
                                                                   US-09-763-397A-22
79
1 SSPSSTKSSPSNVKSP
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ALIGNMENTS

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5	RESULT 1
Searched: 100059 seqs, 36664827 residues	NOA1_HUMAN
	ID NOA1_HUMAN
Total number of hits satisfying chosen parameters: 100059	AC P51513;
	DT 01-OCT-1996 (1

SSPSSTKSSPSNVKSAS 17

Title: Perfect score: Sequence:

Run on:

DB seq length: 0 DB seq length: 200000000 Minimum D Maximum D

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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		Description	P51513 homo sapien	P32323 saccharomyc	P33479 pseudorable		Q62406 mus musculu	O00327 homo sapien	dicty	P28348 emericella	P13653 hordeum vul					9	P53832 saccharomyc	P53301 saccharomyc		Q9z8a6 chlamydia p	O60315 homo sapien	. Q9r0g7 mus musculu	homo sa	gallus	5 gallus	0	N	kluyvei	P13590 gallus gall	homo sa		6	9816	6733 m	P43165 rattus norv
SUMMAKIES		ID	NOA1_HUMAN	AGA1_YEAST	IE18_PRVKA	STE7_YEAST	IRA1_MOUSE	BMAL_HUMAN	RACD_DICDI	NIRA_EMENI	PORA_HORVU	AP1_KLULA	BRC2_HALRO	VTA2_XENLA	IE18_PRVIF	RRA_XENLA	YN23_YEAST	YG46_YEAST	YS8A_CAEEL	CLPC_CHLPN	SIP1_HUMAN	SIP1_MOUSE	N153_HUMAN	TP2B_CHICK	VIT2_CHICK	Y136_TREPA	CP51_USTMA	SEF1_KLULA		AC15_HUMAN	RLR1_YEAST	TR12_HUMAN	ODP2_SCHPO	19KD_MYCAV	CAH5_RAT
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æ	Query	Match	2	٥.	。	59.5	58.2	57.0	55.7	55.7	54.4	54.4	54.4	54.4	53.8	53.2	53.2	53.2	53.2				53.2	53.2	53.2	51.9	51.9	٠.	51.9	-:	51.9		51.3	50.6	50.6
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01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
IMMEDIATE-EARLY PROTEIN 1E180.
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725 AA;
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MISSING (IN ISOFORM 3).
WIIVENS -> KHNISMIS (IN TUMOR ISOFORM).
MISSING (IN TUMOR ISOFORM).
7B9BA8B67CAB6984 CRC64;
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InterPro; IPR000958; KH.

Pfam; PF00013; KH-domain; 3.

PRART; SM00322, KH; 3.

PROSITE; PS50084; KH; TYPE_1; 3.

Nuclear protein; RNA-binding; Repeat; Alternative splicing; Antigen.

DOMAIN 52 87 KH 1.

DOMAIN 177 212 KH 1.

DOMAIN 427 462 KH 3.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-91304412; PubMed-2072914; Roy A., Lu C.F., Marykwas D.L., Lipke P.N., Kurjan J.; Roy A., Lu C.F., Marykwas D.L., Lipke P.N., Kurjan J.; The AGAI product is involved in cell surface attachment of the Saccharomyces cerevisiae cell adhesion glycoprotein a-agglutinin."; Mol. Cell. Biol. 11:4196-4206(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
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Pred. No. 3.9;
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PIR; A41258; A4228.
SGD; S0005377; AGA!
Glycoperotein; Cell adhesion; Signal; GPI-anchor; Repeat;
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01-OCT-1993 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
A-AGGLUTININ ATTACHMENT SUBUNIT PRECURSOR.
AGAI OR YNR044W OR N3431.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           725 AA.
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58.8%;
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                                                                                                                                                             18 X APPROXIMATE TANDEM REPEATS, SER/THR-
RICH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
MEDILINE-91021039; PubMed=2171211;
VICek C., Kozmik Z., Paces V., Schirm S., Schwyzer M.;
Vleck v. Kozmik Z., Paces V., Schirm S., Schwyzer M.;
Pseudorabies virus immediate-early gene overlaps with an oppositely oriented open reading frame: characterization of their promoter and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   enhancer regions.";

virology 179:1656-577(1990).

virology 179:1656-577(1990).

i- FUNCTION: THIS IE PROTEIN IS A MULTIFUNCTIONAL PROTEIN CAPABLE OF MIGRATURG TO THE NUCLEUS, BINDING TO DNA, TRANS-ACTIVATING OF HIGHER VIRAL GENES, AND AUTOREGULATING ITS OWN SYNTHESIS.

-- OTHER VIRAL LOCATION: NUCLEUS OF INFECTED CELLS.

-- PTHA A LONG STRETCH OF SERINE RESIDUES MAY BE A MAJOR SITE OF PHOSPHORYLATION: OTHER ICP4/IE140/IE180 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ô
A-AGGLUTININ ATTACHMENT SUBUNIT.
2 X APPROXIMATE REPEATS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 48; DB 1; Length 725;
Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          70420C853B0B01F8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudorabies virus (strain Kaplan) (PRV).
Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Alphaherpesvirinae; Varicellovirus.
NCBI_TaxID=33703;
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PATHWAY: RESPONSE TO PHEROMONE-INDUCED SIGNAL.
                                                                                                                                                                                                                                                                                                                                                   331
359
363
353
359
363
515 AA;
                                                                                                                                                                                                       S0002318; STE7
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         [2]
SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IRAK1 OR ILIRAK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harrington M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Embryo;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                IRA1_MOUSE
Q62406;
                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                        MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          RESULT 5
IRA1_MOUSE
 셤
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  δ
                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-97127830; PubMed-8972581;
Delaveau T., Blugeon C., Jacq C., Perea J.;
"Analysis of a 23 kb region on the left arm of yeast chromosome IV.";
Yeast 12:1587-1592(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -i- FUNCTION: SERINE/THREDVINE PROTEIN KINASE REQUIRED FOR CELL-TYPE-SPECIFIC TRANSCRIPTION AND SIGNAL TRANSDUCTION IN YEAST. IT IS THOUGHT THAT IT IS PHOSPHORYLATED BY THE STELL PROTEIN KINASE AND THAT IT CAN PHOSPHORYLATE THE FUS3 AND OR KSSI KINASES.

-i- ENZYME REGULATION: PHOSPHORYLATED AT MULTIPLE SITES IN RESPONSE TO PHEROMONE.
                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92331935; PubMed-1628833; Cairns B.R., Ramer S.W., Kornberg K.D.; Order of action of components in the yeast pheromone response pathway revealed with a dominant allele of the STE11 kinase and the multiple phosphorylation of the STE7 kinase."; Genes Dev. 6:1305-1318(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-87016949; PubMed-3532111;
Teague M.A., Chaleff D.T., Errede B.;
Nucleotide sequence of the yeast reaulatory gene STE7 predicts a protein homologous to protein kinases.";
Proc. Natl. Acad. Sci. U.S.A. 83:7371-7375(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE-94178255; PubMed-8131746;
Zheng C.-F., Guan K.-L.;
"Activation of MEK family kinases requires phosphorylation of two
                                                                                                                                                                                                                                                                                                                                                  Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                        ö
                                           Early protein; Transcription regulation; Trans-acting factor; DNA-binding; Phosphorylation; Nuclear protein.

DOMAIN 347 354 POLY-SER.
                                                                                                                                 Score 48; DB 1; Length 1446;
Pred. No. 16;
2; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PHOSPHORYLATION SITES SER-369 AND THR-373, AND MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                              81F43A3DE3DDA068 CRC64;
                                                                                                                                                                                                                                                                                      01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
01-JAN-1980 (Rel. 39, Last annotation update)
SERINE/THREONINE PROFILE KINASE STE7 (EC 2.7.1.-).
STE7 OR YDL159W OR D1525.
                                                                                                                                                                                                                                                                   515 AA
 or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                   PRT;
                                                                                              1446 AA; 148640 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           conserved Ser/Thr residues.";
EMBO J. 13:1123-1131(1994).
                      EMBL; M34651; AAA47470.1; -.
                                                                                                                               60.8%;
64.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE OF 70-515 FROM N.A.
                                                                                                                                                                                                       842 SSPASTKSSSSTKSSSS 858
                                                                                                                                                                               1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                 Query Match 60.8
Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                                                                                                  STANDARD;
                                                                                  397
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-S288C / FY1679;
                                   A45344; A45344.
                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               POSSIBLE FUNCTION.
                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-S288C;
Pohl T.M.;
                                                                                                                                                                                                                                                                 STE7_YEAST
P06784;
                                                                                              SEQUENCE
                                                                                  DOMAIN
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostoml;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES. MAP KINASE KINASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
INPERLEUKIN-1 RECEPTOR-ASSOCIATED KINASE 1 (EC 2.7.1.-) (IRAK-1)
(IRAK) (PELLE-LIKE PROTEIN KINASE) (MPLK).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             InterPro; IPR00019; Euk_pkinase.
InterPro; IPR002290; Ser_thr_kin_actsite.
Pfam; PF00069; pkinase; 1.
PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00108; PROTEIN_KINASE_ATP; 1.
PROSITE; PS00101; PROTEIN_KINASE_DOM; 1.
Transferase; Serine/threonine-protein kinase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 515;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4; Indels
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Kopp E.B., Ghosh S.;
"Cloning of mouse IRK.";
submitted (NOV-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                S->A: NO LOSS OF ACTIVITY.
S->A: INACTIVATION.
T->A: INACTIVATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C8A75899CFBE8BDE CRC64;

        Phosphorylation;
        Pheromone response.

        DOMAIN
        191
        466
        PROTEIN KINASE.

        NP_BIND
        197
        205
        ATP (BY SIMILARITY.)

        BINDING
        220
        ATP (BY SIMILARITY.)

        ACT_SITE
        331
        BY SIMILARITY.)

        MOD_RES
        359
        359
        PHOSPHORYLATION.

        MOD_RES
        363
        PHOSPHORYLATION.

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 47; DB 1;
Pred. No. 7.7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             710 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   205
220 A:
220 A:
331 B:
359 P:
363
363
363 C:
57709 MW;
                                                                                                                                                                                                                                                                                                                                                          EMBL; M14097; AAA35118.1; -. EMBL; Z67750; CAA91587.1; -. EMBL; Z74207; CAA98732.1; -. EMBL; X97751; CAA66332.1; -. PIR; A25048; A25048
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          59.5%;
56.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE OF 34-710 FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          130 SPSSTNSTPSTIQGLS 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 SPSSTKSSPSNVKSAS 17
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TAMENT TO THE SECOND TO THE SECOND TO THE SECOND TO THE SECOND THE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BMAL, HUMAN STANDARD: PRT; 583 AA. 199649; 000337; 000318; 000317; 099649; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-JUL-1999 (Rel. 38, Last annotation update) BMALI PROFEIN (BRAIN AND MUSCLE ARNT-LIKE I) (MEMBER OF PAS PROTEIN 3) BMALI OR ARNTL.
                                                                                         THE IL-1 RECEPTOR ILL-R-1. PATHWAY. THIS KINASE ASSOCIATES WITH THE IL-1 RECEPTOR ILL-R-1. THIS ASSOCIATION IS RAPID AND IL-1 DEPENDENT US SIMILARITY).

-1 TISSUE SPECIFICITY: HIGHLY EXPRESSED IN LIVER, FOLLOWED BY KIDNEY AND SKELETAL MUSCLE.
-1 DEVELOOMBRATE. STAGE: EXPRESSED FROM E11 DAY TO E18 DAY.
-1 PTM: AUTOPHOSPHORYLATED. AN EXTENSIVE PHOSPHORYLATION OF IRAK OCCURS AFTER ITS ASSOCIATION WITH ILL-R-1. THIS STEP COULD BE LINKED TO THE ACTIVATION OF THE KINASE (BY SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING (ISOFORMS BMALL A-F).
                    Trofimova M., Sprenkle A.B., Green M., Sturgill T.W., Goebl M.G., Harrington M.A.; "Developmental and tissue-specific expression of mouse pelle-like protein kinase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homon sapiens (Human).
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A Frank Pro0069; pkinase; 1.

R PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

R PROSITE; PS001019; PROTEIN_KINASE_ST; 1.

R PROSITE; PS001019; PROTEIN_KINASE_DOM; 1.

R PROSITE; PS001019; PROTEIN_KINASE_DOM; 1.

RW Transferase; Serine-threonine-protein kinase; ATP-binding.

FT DOMAIN 212 521 ATP (BY SIMILARITY).

FT NP_BIND 218 226 ATP (BY SIMILARITY).

FT BINDING 239 239 ATP (BY SIMILARITY).

FT SITE 338 338 BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE-Brain;
MEDLINE-7289529; PubMed=9144434;
MEDLINE-7289529; Missue-specific expression of a novel basic "cDNA cloning and tissue-specific expression of a novel basic helix-loop-helix/PAS protein (BMALI) and identification of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Score 46; DB 1; Length 710;
Pred. No. 15;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL, U56773; AAC52694.2; -.
EMBL; AF103876; AAD3324.1; ALT_INIT.
MGD; MG1107420; 111rav.
InterPro; IPR000719; Euk_pkinase.
InterPro; IPR002290; Ser_thr_kin_actsite.
  MEDLINE=96279287; PubMed=8663605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 58.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 SSPSSTKSSPSN 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity
Matches 9; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
BMAL_HUMAN
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The interactivety spiced variants with alternative translation

Hittation General vety spiced variants with alternative translation

Hittation General Paris Commun. 231.258-264(1997).

MARCHES-FEELD BAIS NA. (ISOPONH MOR3).

HIGHER-FEELD BAIS NA. (ISOPONH MOR3).

HIGHER CIRCLASS NA. (ISOP
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and for commercial

Usage by

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(See http://www.isb-sib.ch/announce/
                                                                                                                                                                     EFFECTOR REGION (POTENTIAL).
POLY-VAL.
POLY-THR.
                                                                                                                                                                                                               6CA47BFDA2626BC4 CRC64;
                                                                                                                                       SIMILARITY).
SIMILARITY).
SIMILARITY).
                                                                                                                                                                                                                                              Score 44; DB 1;
Pred. No. 10;
2; Mismatches
 modified and this statement is not removed. entities requires a license agreement (See hor send an email to license@lsb-sib.ch).
                                                                                                                                                              (BY
                                                                                                                                                                                                      POLY-SER
                                                                                                                                                  (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001138; Zn2_CY6_fungal.
Pfam; PF00172; Zn_clus; 1.
                                                                                                                                                                                                                                                                                                                                                                PRT;
                                                                                  Interpro; IPR001806; Ras_trnsfrmng.
Interpro; IPR003578; Rho.
                                                                                                                                       GTP (GTP (GTP (
                                                                                                                                                                                                                                                                    5;
                                         EMBL; AF310889; AAG45121.1; -.
                                                                                                                                                                                                                 X.
                                                                                                                                                                                                                                               55.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; M68900; AAA33317.1; -.
                                                                                                                                                                                                                                                                                                       198 SSPSSTSSKPSKTTTT 214
                                                     EMBL; L11594; AAC37390.1;
HSSP; P21181; 1AM4.
                                                                                                                                                                                                                27530
                                                                                                                                                                                                                                                                                         1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                       Pfam; PF00071; ras; 1.
SMART; SM00174; RHO; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PIR; A41697; A41697.
HSSP; P08657; 1CLD.
                                                                                                                                                                                                                                                       Similarity
9; Conserva
                                                                                                                                                                                         210
217
254 AA;
                                                                      DictyDb; DD05066;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5072;
                                                                                                                 SMART; SM001'
GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                NIRA_EMENI
P28348;
                                                                                                                                                                                                                SEQUENCE
                                                                                                                                                                                                                                               Query Match
Best Local 3
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                                                                                ISOPORM MOP3).

T -> R (IN ISOPORM BMALIC).
MISSING (IN ISOPORM BMALIC).
MISSING (IN ISOPORM BMALID).
SFCTIHSTGXLKSWPPTKMGLDED -> AFCTIHSTGYFGI
FTTRTSRHIYU. (IN ISOPORM BMALIE).
MISSING (IN ISOPORM BMALIE).
ANVLEGGDPFPOLTASPHSKNDSMLPSGEGPRTHPTVPG
IPGGTRAGAGKIGRNIAEEIMEIHRIRGSSPSSCGSSPLNI
                                                                                                                                                                              TS -> SRVDTGHLGQVERCTVLSRPNSRFLIAGMFTEPTS
WARGTQPSSGHPSTWARACCPLEKVAQRGPTPLFQGFQG
EPGLGGEK (IN ISOFORM BMALIF).
MISSING (IN ISOFORM BMALIF).
                                                            MINIESMDTDKDDPHG -> MSKEAVSLWALTVSLOPPVPL
CVCREMTGSGRRKQQCVTLPPISRELCFYLLLFPPP (IN
                                           -> MADQRMDISSTISDFMSPGPTDLLSSSLGTSGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bush J.M. IV. Franck K., Cardelli, J.A.; Cardelli, J.A.; "Cloning and characterization of seven novel Dictyostellum discoideum rac-related genes belonging to the rho family of GTPases."; Gene 136:61-66(1993).
                                                                                                                                                                                                                                                                                                                                                        Gaps
  HELIX-LOOP-HELIX MOTIF (BY SIMILARITY).
                                                     DCNRKRKGSSTDYQ (IN ISOFORM BMAL1B).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rivero F., Dislich H., Glockner G., Noegel A.A.; "The Dictyostellum discoideum family of Rho-related proteins."; Nucleic Acids Res. 29:1068-1079(2001).
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                                                                                                                                                                                                                                                                                                                                 Length 583;
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                                                                                                                                                                                                                                                                                        -> LR (IN REF. 2).
2AA8E7EEB4A71119 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Mycetozoa; Dictyosteliida; Dictyostellum.
NCBI_TaxID-44689;
                                                                                                                                                                                                                        R -> G (IN REF. 2).
K -> K (IN AB000B12).
S -> P (IN AB000B12).
K -> N (IN AB000B15).
D -> N (IN AB000B15).
S -> N (IN AB000B15).
SP -> LR (IN REF. 2).
                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           P34150; Q9GPS8;
01-FFB-1994 (Rel. 28, Created)
0-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    254 AA
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                                                                                                                                                                                                                                                                                                                                  Score 45;
Pred. No.
                                PAC MOTIF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Dictyostelium discoideum (Slime mold)
                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
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MEDLINE=21127961; PubMed=11222756;
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MEDLINE-94124042; Pubmed-8294042;
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66.7%;
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 83
170
351
401
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483
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583 AA;
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Best Local Similarity
Matches 10; Conserv
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231
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Gaps

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Indels

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Length 254;

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between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration
                                                                                                                                                                                                                                                                          Emericella nidulans (Aspergillus nidulans).
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Eurotiomycetes;
Eurotiales; Trichocomaceae; Emericella.
01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
01-APR-1993 (Rel. 25, Last annotation update)
NITROGEN ASSIMILATION TRANSCRIPTION FACTOR NIRA.
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AP1_KLULA
P56095;
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BRC2_HALRO
ID BRC2_HA
AC 001409
DT 01-NOV
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"Nucleotide sequence of a cDNA coding for the NADPH-
protochlorophyllide oxidoreductase (PCR) of barley (Hordeum vulgare
protochlorophyllide oxidoreductase (PCR) of barley (Hordeum vulgare
L) and its expression in Escherichia coll.";
Mol. Gen. Genet. 217:355-361(1989).
-1- FUNCTION: PHOTOTRANSFORMATION OF PROTOCHLOROPHYLLIDE (PCHLIDE) TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CHLOROPHYLLIDE (CHLIDE).
CATALUTIC ACTIVITY: CHLOROPHYLLIDE A + NADP(+) =
PROTOCHLOROPHYLLIDE + NADPHYLLIDE + NADPHYLLIDE + NADPHYLLIDE
PATHWAY: CHLOROPHYLL BIOSYWHESIS.
SUBCELLUIAR LOCATION: CHLOROPLAST.
BUYELDEMBRYATA, STAGE: ACTIVE ONLY TRANSIENTLY IN ETIOLATED
SEEDLINGS AT THE BECINNING OF ILLUMINATION.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Hordeum vulgare (Barley).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta: Liliopsida; Poales; Poaceae; Pooldeae;
Triticeae; Hordeum.
                                                                                                                                                                                                                                                                                                                                                                         01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-JAN-1990 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROTOCHLOROHYLLIDE REDUTASE A, CHLOROPLAST PRECURSOR (EC 1.3.1.33)
(PCR A) (NADPH-PROTOCHLOROPHYLLIDE OXIDOREDUCTASE A) (POR A).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Schuelz R., Steinmueller K., Klaas M., Forreiter C., Rasmussen S.,
Hiller C., Apel K.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; X15869; CAA33879.1; -.
PIR; S04783; S04789; APL-short.
Pfan: PF00106; adh.short; 1.
Photosynthesis: Chlorophyll biosynthesis; Oxidoreductase; NADP; Chlorophyll biosynthesis; Oxidoreductase; NADP; Chlorophyll biosynthesis; Oxidoreductase; NADP; Chlorophiast; Transit peptide; Multigene family.
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Pred. No. 37;
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                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A., AND PARTIAL SEQUENCE. STRAIN-CV. CARINA; TISSUE-Leaf; MEDLINE-89364719; PubMed=2671659;
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                                                                                                                                                                                                     Query Match
Best Local Similarity 52.9%;
Matches 9; Conservative
                                                                                                                                                                                                                                                                                 652 ASPSTISDSPPSVSSQS 668
                                                                                                                                                                                                                                                         1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                    STANDARD;
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NCBI_TaxID=4513;
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P13653;
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MEDIATE-98410743; PubMed=9439570;

MEDIATE-98410743; PubMed=9439570;

"Characterization of an AP-1-like transcription factor that mediates an oxidative stress response in Kluyveromyces lactis.";

MOI, Gen. Genet. 257:62-70(1997).

-1- FUNCTION: MEDIATES OXIDATIVE STRESS RESPONSE. INVOLVED IN BOTH THE OXIDATIVE ND CADMIUM RESPONSE PATHWAYS.

-1- SUBJECTULIAR LOCATION: NUCLEAR.

-1- SIMILARITY: TO OTHER BZIP PROTEINS.
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PROSTIE; PS00036; BZIP_BASIC; 1.
Transcription requiation; DNA-binding; Activator; Nuclear protein.
DNA_BIND 67 BASIC MOTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Kluyveromyces lactis (Yeast).
Eukaryota: Pungi, Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaces; Kluyveromyces.
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CHLOROPLAST.
PROTOCHLOROPHYLLIDE REDUCTASE.
EBD3EF153D96C129 CRC64;
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                                                                                                           Length 388;
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A4A96B12D7F5C983 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
15-JUL-1999 (Rel. 38, Last annotation update)
AP-1-LIKE TRANSCRIPTION FACTOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 43; DB 1
Pred. No. 34;
2; Mismatches
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22;
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Pred. No.
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                                           41181 MW;
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58.8%;
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ilarity 60.0%;
Conservative
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Matches 10; Conservative
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75 3
388 AA;
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Best Local Similarity
Matches 9; Conserv
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NCBI_TaxID=8355
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                                                                                                                                                               **MEDLINE=97115721; PubMed=8954744;

**ABDLINE=97115721; PubMed=8954744;

**Yasuo H., Kobayashi M., Shimauchi Y., Satoh N.;

**The ascidlan genome contains another T-domain gene that is expressed in differentiating muscle and the tip of the tail of the embryo.";

**In differentiating muscle and the tip of the tail of the embryo.";

**Dev. Biol. 180:773-779(1996).

**In Dev. Biol. 180:773-779(1996).

**In Dev. Biol. 180:773-779(1996).

**In Tail CALLED T SITES AND ACTIVATES GENE TRANSCRIPTION WHEN BOUND TO SUCH A SITE (BY SIMILARITY).

**In SUBCLIVILAR LOCATION: NUCLEAR (POTENTIAL).

**In SUBCLIVILAR LOCATION: NUCLEAR (POTENTIAL).

**In SUBCLIVILAR LOCATION: NUCLEAR (POTENTIAL).

**In SUBCLIVILAR STAGE: FIRST PETECTED IN THE VEGETAL HEMISPHERE AT TISSUE SPECIFICITY: DIFFERENTIATING MUSCLE AND BECOMES EVIDENT THE 32-CELL STAGE: EXPRESSION CONTINUES IN ENDOTHELIAL LINEAGE UNTIL 110-CELLS EXPRESSION INCREASES THROUGHOUT

**IN MUSCLE LINEAGE CELLS: EXPRESSION IN CREASES THROUGHOUT

**IN MUSCLE LINEAGE CELLS: EXPRESSION ALSO DETECTED IN THE TAILBUD

**IT FROM MID-GASTRULATION ALSO DETECTED IN THE TAILBUD

**IT FROM MID-GASTRULATION TO TAIL ELONGATION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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P18709; Q11895;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 16, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
VITELLOGENIN A2 PRECURSOR (VTG A2) [CONTAINS: LIPOVITELLIN I;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE: PS01283: TBOX_1: 1.
PROSITE: PS01264; TBOX_2: 1.
PROSITE: PS50252; TBOX_3: 1.
Developmental protein: Transcription regulation; DNA-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 681;
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                                                                             Eukaryota; Metazoa; Chordata; Urochordata; Ascidiacea;
Stolidobranchia; Pyuridae; Halocynthia.
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40;
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
T-BOX CONTAINING PROTEIN 2 (AS-T2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mismatches
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                                                             Halocynthia roretzi (Sea squirt).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              76430 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR01699; T-box. Pfam; PF00907; T-box. 1. PRINTS; PR00937; TBOX. SMART; SM00425; TBOX: 1.
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Matches 9; Conserv
                                                                                                        NCBI_TaxID=7729;
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VTA2_XENLA
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-i- INDUCTION: VITELLOGENIN IS SYNTHESIZED IN THE LIVER OF OVIPAROUS YERTERARTES IN RESPONSE TO STEROID (ESTROGEN) INDUCTION.
-i- MISCELLANEOUS: THE SERINE-RICH PORTION OF VITELLOGENIN ENCODES PHOSYTTIN (OR TWO PROSYETTES). IT IS ASSUMED TO BE PHOSPHORYLATED TO A LEVEL OF ABOUT 80%.
                                                                                                                                                                                                                                                                                                                                                                                   Gerber-Huber S., Nardelli D., Haefliger J.-A., Cooper D.N., Givel F., Germond J.-E., Engel J., Green N.M., Wahli W.;

"Precursor-product relationship between vitellogenin and the yolk proteins as derived from the complete sequence of a Xenopus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDITER-88058863; PubMed=3680202;
Nardelli D., Het Schip F.D., Gerber-Huber S., Haefliger J.A., Gruber M., Ab G., Wahli W.;
"Comparison of the organization and fine structure of a chicken and Yenopus laevis vitellogenin gene.";
J. Biol. Chem. 262:15377-15385(1987).
                                    Xenopus laevis (African clawed frog).
Sukaryota Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 1-72 FROM N.A. MEDLINE-85062836; PubMed=6504705; Walker P., Germond J.-E., Brown-Luedi M., Givel F., Wahli W.; Walker P., Germond J.-E., Brown-Luedi M., Givel F., Wahli W.; Sequence homologies in the region preceding the transcription initiation site of the liver estrogen-responsive vitellogenin and apo-VLDLII genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Wallace R.A., Hoch K.L., Carnevali O.; "Placement of small lipovitellin subunits within the vitellogenin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEIC ACIGS RES. 12:8611-8626(1984).
-!- FUNCTION: PRECURSOR OF THE MAJOR EGG-YOLK PROTEINS THAT ARE SOURCES OF NUTRIENTS DURING EARLY DEVELOPMENT OF OVIPAROUS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Storage protein; Phosphorylation; Signal; Glycoprotein.
PHOSVETTE I; PHOSVETTE II].
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A., AND SEQUENCE OF 16-28.
MEDLINE=87259958; PubMed=3601655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 15:4737-4760(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; S03124; S03124.
PIR; S10652; S10625; S10625.
InterPro; IPR001747; Vitellogenin_N.
InterPro; IPR001846; Vwd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 1291-1302.
MEDLINE-90278951; PubMed-2352275;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF01347; Vitellogenin_N; 1. Pfam; PF00094; vwd; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              scursor in Xenopus laevis.";
Mol. Biol. 213:407-409(1990).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; Y00354; CAA68433.1; -. EMBL; M18061; AAA49982.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X00205; CAA25028.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        vitellogenin gene.'
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Gaps

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2; Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PUTCO. Natl. Acad. Sci. U.S.A. 89:2321-2325(1992).

-!- FUNCTION: THIS IS A RECEPTOR FOR RETINDIC ACID. THIS METABOLITE
HAS PROFOUND EFFECTS ON VERTEBRATE DEVELOPMENT. RETINDIC ACID IS
A MORPHOGEN AND IS A POWERFUL TERATOGEN. THIS RECEPTOR CONTROLS
CELLS FUNCTIONS BY DIRECTLY RECULATING GENE EXPRESSION.
-!- SUBCELLULAR LOCATION: NUCLEAR.
-!- DEVELOPMENTAL STAGE: IT IS SYNTHESIZED DURING OOGENESIS AND
PERSISSI IN THE CLEAVING EMBRYO AT APPROXIMATELY CONSTANT LEVELS
UNTIL IT IS DEGRADED JUST BEFORE GASTRUATION.
-!- DOMAIN: COMPOSED OF THREE DOMAINS: A MODULATING N-TERMINAL DOMAIN.
-!- SIMILARITY: BELONGS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
-!- SIMILARITY: PRECNICS TO THE NUCLEAR HORMONE RECEPTORS FAMILY.
NR1 SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.

BLUINE-2196110; PubMed-1312717;
BLUINE-2196110; NubMed-1312717;
BLUINE-2196110; Mangelsdorf D.J., Dyck J.A., Bittner D.A., Evans R.M.,
BLUINE-15 E.M.;
Miltiple retinoid-responsive receptors in a single cell: families of retinoid 'X' receptors and retinoic acid receptors in the Xenopus
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Cranidea; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
Xenopodinae; Xenopus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FIGURE: PROGOST, STEED FROM PER.
PRINTS: PROGOST STEED FROM PER.
PRINTS: PROJECT STEED FROM PER.
SMART: SMOOST PER.
SMART: SMOOST PER.
SMART: SMOOST PER.
SMART: SMOOST STEED FROM PER.
RECEPTOR: PROGETTE: PSOOOT: WICLERA RECEPTOR; 1.
RECEPTOR: Transcription regulation; DNA-binding; Nuclear protein;
Zinc-finger: Multigene family.
DOMAIN
                 DB 1; Length 1461;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MODULATING (BY SIMILARITY).
NUCLEAR RECEPTOR-TYPE.
C4-TYPE.
               Score 42.5; DB 1
Pred. No. 1e+02;
                                                                                                                                                                                                           01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
01-0CT-1996 (Rel. 34, Last senderation update)
RETINOIC ACID RECEPTOR ALPHA (RAR-ALPHA).
                                                                                                                                                                                 458 AA.
                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           HASSY, PLUGACA, LHRA.
INTERPRO; IPPRO00536; Hormone_rec_lig.
INTERPRO; IPPR001723; Strdhormone_reptor.
InterPro; IPPR001688; Zf-C4.
Pfam; PP00104; hormone_rec; 1.
Pfam; PF00105; Zf-C4; 1.
                                                                                                                                                                                                                                                                                        Xenopus laevis (African clawed frog)
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HSSP; P10826; 1HRA.
                                                                                            853 SSPASTKSG-SSTKSSS 868
                                                                         1 SSPSSTKSSPSNVKSAS 17
                 Query Match
Best Local Similarity 64.7
Matches 11; Conservative
                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=8355;
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                                                                                                                                                                                 RRA_XENLA
P51126;
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ZN_FING
ZN_FING
                              Best Loca
Matches
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                                                                                                                                                                  RRA_XENLA
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POLY SER.
POLY SER.
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POLY SER.
N-LINKED (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      of
                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pseudorabies virus (strain Indiana-Funkhauser / Becker) (PRV). Viruses; daDNA viruses, no RNA stage; Herpesviridae; Alphaherpesvirinae; Varicellovirus. NCBI_TaxID=31523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cheung A.K.; "DNA nucleotide sequence analysis of the immediate-early gene
 PHOSVITIN (OR PHOSVETTES I + II).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Early protein; Transcription regulation; Trans-acting factor; DNA-binding; Phosphorylation; Nuclear protein.

390 405 POLY-SER.
                                                                                                                                                                                                                                          Length 1807;
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• V (IN REF. 4).
D109BBF568147742 CRC64;
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149833 MW; 7F31E7ABE403B208 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- SIMILARITY: BELONGS TO THE ICP4/IE140/IE180 FAMILY.
                                                                                                                                                                                                                                           Score 43; DB.1; I
Pred. No. 1.1e+02;
                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0CT-1989 (Rel. 12, Created)
01-AFR-1990 (Rel. 14, Last sequence update)
01-FEB-1994 (Rel. 28, Last annotation update)
IMMEDIATE-EARLY PROTEIN IE180.
               LIPOVITELLIN II. SER-RICH.
                                                                                                                                                                                                                                                                                                                                                                                                             PRT; 1461 AA.
                                                                                                                                                                                                                                                                          Mismatches
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MEDLINE-89315207; Pubmed=2546124;
                                                                                                                                                                                               201544 MW;
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                                                                                                                                                                                                                                           54.4%;
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                                                                                                                                                                                                                                                                                                       1 SSPSSTKSSPSNVKSAS 17
                                                                                                                                                                                                                                          Query Match 54.4
Best Local Similarity 58.8
Matches 10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
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11179
11205
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1309
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1807
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P11675;
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DOMAIN
SEQUENCE
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Messenguy F., Dubois E., Vierendeels F., Scherens B., Pierard A.,
Glansdorff N.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GLCNAC. . .) (POTENTIAL).
D (GLCNAC. . .) (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                          Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
NCBI_TaxID=4932;
                                                                                                                                                                                                                                                             01-0CT-1996 (Rel. 34, Created)
01-0CT-1996 (Rel. 34, Last sequence update)
15-JUL-1998 (Rel. 36, Last annotation update)
HYPOTHETICAL 52.3 KDA PROTEIN IN MRPL10-ERG24 INTERGENIC REGION
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             LIGAND-BINDING (BY SIMILARITY). 4D80BB18678B1E17 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           n; Transmembrane; Signal.

23 POTENTIAL.

803 HYPOTHETICAL PROTEIN YNL283C.

81 POTENTIAL.

346 N-LINED (GLCNAC. . ) (POTENTIAL.

429 N-LINED (GLCNAC. . ) (POTENTIAL.

483 N-LINED (GLCNAC. . ) (POTENTIAL.

483 N-LINED (GLCNAC. . ) (POTENTIAL.

483 N-LINED (GLCNAC. . ) (POTENTIAL.

484 N-LINED (GLCNAC. . ) (POTENTIAL.

485 N-LINED (GLCNAC. . ) (POTENTIAL.

486 N-LINED (GLCNAC. . ) (POTENTIAL.

487 N-LINED (GLCNAC. . ) (POTENTIAL.
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Pred. No. 41;
3; Mismatches 5; Indels
                                                                       Length 458
                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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                                                                      Score 42; DB 1;
Pred. No. 37;
0; Mismatches
                                                                                                                                                                                                                                     503 AA
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HINGE.
                             50573 MW;
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SGD; SO005227; YNL283C.
InterPro; 1PR002899; WSC.
Pfam; PF01822; WSC; 1.
SMART; SM00321; WSC; 1.
Hypothetical protein; Transmem SIGNAL
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                                                                      Query Match 53.2%;
Best Local Similarity 90.0%;
Matches 9; Conservative
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154 1
200 4
458 AA;
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326
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503 AA;
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445 SPSSTHSSPS 454
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Best Local Similarity
Matches 9; Conserv
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                                                                                                                                                                                                                                   YN23_YEAST
P53832;
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DOMAIN
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YN23_YEAST
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Search completed: January 29, 2002, 11:16:19

qq

us-09-763-397a-22.rspt

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Q9y4s1 homo sapien Q91hf0 arabidopsis Q9p2f8 homo sapien Q91pe8 arabidopsis Q14947 schizosacch Q9yaal leishmania Q88337 rattus norv Q9rOuz mus musculu Q88295 mus musculu Q8810 rattus norv Q9xcl8 mus musculu Q8810 rattus norv Q9xcl8 mesocricetu Q8810 rattus norv Q9xcl8 mesocricetu Q8417 qailus qa
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Q9uix6 homo sapien
Q9m9u2 arabidopsis
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Ol6139 lytechinus
Oghedl neurospora
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN-SIERRA LEONE;
MEDLINE-93293317; PubMed-7685740;
Howard R.F., Jensen J.B., Franklin H.L.;
"Reactivity profile of human anti-82-kilodalton rhoptry protein antibodies generated during natural infection with Plasmodium falciparum.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Last annotation update)
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Mol. Biochem. Parasitol. 51:327-330(1992)
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EMBL: L10322; AAB59202.1; -.
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STRAIN-SIERRA LEONE;
MEDLINE-92244303; Pubmed-1574089;
                                                                                                    01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08,
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SEQUENCE FROM N.A.
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       NON_TER
SEQUENCE
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Q26002;
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Q26002
     qq
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Q98tq9 gallus gall
Q9pab6 xylella fas
Q9y1j5 dictyosteli
Q9qy63 mus musculu
                                                                                                                                                                                             (without alignments)
39.615 Million cell updates/sec
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                                                                                                                                                                        Search time 62.77 Seconds
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                           GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       hits satisfying chosen parameters:
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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"The sequence of the p82 rhoptry protein is highly conserved between two Plasmodium falciparum isolates.";
two Plasmodium falciparum isolates.";
EMB1. Biochem. Parasitol. 51:327-330(1992).
EMB5. MB0807; AAA2911.;
SEQUENCE 782 AA, 90096 MW; D1AD099862528D42 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ridley R.G., Takacs B., Lahm H.W., Delves C.J., Goman M., Certa V., Matlle H., Woollett G.R., Scalfe J.G.;
"Characterisation and sequence of a protective rhoptry antigen from Plasmodium falciparum.";
Mol. Blochem. Parasitol. 41:125-134(1990).
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Pred. No. 0.0059;
0; Mismatches 0; Indels
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
RHOPTRY ASSOCIATED PROTEIN 1 (ROP1) PRECURSOR (FRAGMENT).
PLASMOCIMM falciparum.
Bukaryota; Alveclata; Apicomplexa; Haemosporida; Plasmodium.
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90080 MW; ZFZE240D40A4C902 CRC64;
                                                                                                                                                                                                                                                            01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-VUN-2000 (TrEMBLrel. 14, Last annotation update)
PR86 RHOPTRY PRECURSOR PROTEIN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-HONDURAS I CDC;
MEDLINE-90348711; PubMed=2200961;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [2]
SEQUENCE FROM N.A.
STRATN=HONDURAS I CDC;
MEDLINE=92244303; Pubmed=1574089;
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MEDLINE=90348711; Pubmed=2200961;
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94.48;
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145 SSPSSTKSSSPSNVKSAS 162
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Best Local Similarity 94.4'
Matches 17; Conservative
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782 AA;
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SEQUENCE
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Q26007;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "The sequence of the p82 rhoptry protein is highly conserved between two Plasmodium falciparum isolates."; Mol. Biochem. Parasitol. 51:327-330(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ,Gaps
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Pred. No. 0.0015;
0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                              Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota: Alveolata: Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=5837;
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Submitted (FE11995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20985: AAAA3681.1; SEQUENCE 782 AA, 90023 MW; F69E26A2A564C8EA CRC64;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-MAK-2001 (TrEMBLrel. 16, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN-1.
                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
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EMBL; L10323; AAA29742.1; -.
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STRARTAFARZANIA I/CDC;
MEDILINE-92244303; PubMed-1574089;
HOWAIR R.F.
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Best Local Similarity 94.4%;
Matches 17; Conservative
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026003
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782 AA.

DB 5; Length 782;

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"Efficacy of vaccines containing Rhoptry-Associated Proteins RAP1 and RAP2 of Plasmodium falatiparum in Saimiri boliviensis monkeys."; Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases. EMBL, AF205284; AAF23405.11
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Plasmodium reichenowi.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                        Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                              5; Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AF206631; AAF15365.1; -
SEQUENCE 782 AA; 90082 MW; 8E1F4CF2883903FD CRC64;
                                                                                                                                                                                                                                                                                                                                            3284; AAF23405.1; -.
782 AA; 90041 MW; 27F2EA9BC930434E CRC64;
                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY-ASSOCIATED PROFEIN 1.
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
RHOPTRY ASSOCIATED PROFEIN 1.
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN-1.
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Best Local Similarity 94.4
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                    PRELIMINARY;
                                                                                                                                                                       Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. STRAIN=FCC1/HN;
                                                                                                                                                                                                                                      SEQUENCE FROM N.A. STRAIN=FVO;
                                                                                                                                                                                                     NCBI_TaxID=5833;
                                                                                                                                                                                        Eukaryota;
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
                                                                                                                                                                                                                                                                         Saul A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q26104
Q26104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q9U414
Q9U414;
                                                   Q9U429
Q9U429;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             RESULT 10
025104
AC 025104
AC 025104
DT 01-NOV
DT 01-NOV
DT 01-JUN
DE RHOPTR'
GN RAP-1.
OS PLASTMON
OC RUKATYN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6
                     RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT
                                    090429
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   090414
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                QQ
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                    ï
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
                                                                                                                                                                                                                                                                                                                                                                                        Saul A.;
"Efficacy of vaccines containing Rhoptry-Associated Proteins RAP1 and "RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF205282; AAF23403.1; ...
NON_TER 782 AA: 90066 MW; B344948D5806F7DC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Saul A.;
"Efficacy of vaccines containing Rhoptry-Associated Proteins RAP1 and
RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF205283; AAF23404.1;
NON_TER 782 782
                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ï
                                    ;;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5; Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             86.7%; Score 68.5; DB 5; Length 782; 94.4%; Pred. No. 0.0059; 1ve 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                    Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
NCBL_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
94.4%; Pred. No. 0.0059;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           782 AA; 90131 MW; A0FCB64529C34E59 CRC64;
                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-MAY-2000 (TrEMBLrel. 13, Created)
U-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 68.5; DB 5
Pred. No. 0.0059;
0; Mismatches
                                                                                                                                                                                       782 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     782 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ·.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   145 SSPSSTKSSSPSNVKSAS 162
                                                                                    SSPSSTKSSSPSNVKSAS 162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSPSSTK-SSPSNVKSAS 17
                                                                  1 SSPSSTK-SSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 SSPSSTK-SSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 94.4'
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Best Local Similarity 94.4
Matches 17; Conservative
                                 17; Conservative
                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
                                                                                                                                                                                                                                                                                                         Plasmodium falciparum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmodium falciparum
                 Best Local Similarity
Matches 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-FUP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                                                                                                       090431;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9U430;
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RESULT Q9U430

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Gaps

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Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
              δλ
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Brosophila metanogaster (Fruit fly).
Eukaryota: Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota: Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "The sequence of the p82 rhoptry protein is highly conserved between two Plasmodium falciparum isolates."; MOI. Blochem. Parasitol. 51:327-330(1992).
                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Howard R.F., Peterson C.; "Limited RAP-1 sequence diversity in field isolates of Plasmodium "Limited RAP-1 sequence diversity in field isolates of Plasmodium "Mol Biochem." Parasitol. 77:95-98(1996).

EMBL; U41074; AAC47090.1; ".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲;
                                                                                                                                                                                                                                           1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 62.5; DB 5; Length 292;
Pred. No. 0.022;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-UNV-2000 (TrEMBLrel. 14, Last annotation update)
STRAIN INDD RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
                                                                                                                                                                                                   5; Length 782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1; Indels
                                                                                                                                                                                                                                           0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 292 292
292 AA; 32345 MW; A35C979C3FEC3019 CRC64;
                                                                                 Shi Y., Lal A.A.;
Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                EMBL; U20986; AAA63682.1; -.
SEQUENCE 782 AA; 90160 MW; DE6D1BE2FAC308A9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
RHOGEF2 PROTEIN.
                                                                                                                                                                                                   Score 65.5; DB 5
Pred. No. 0.018;
1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2559 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                           292 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-INDD (INDIAN ISOLATE D);
MEDLINE-96379224; PubMed-8784775;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=INDD (INDIAN ISOLATE D);
MEDLINE=92244303; PubMed=1574089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     79.1%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      139 SSPSITKSSSPSNVKSAS 156
                                                                                                                                                                                                           82.9%;
88.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSPSSTK-SSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                              145 SSPSSTKSSSPSNVKTAS 162
                                                                                                                                                                                                                                                                                       1 SSPSSTK-SSPSNVKSAS 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                             Query Match 82.99
Best Local Similarity 88.99
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RHOGEF2 OR CG9635.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                         SEQUENCE FROM N.A.
                                 NCBI_TaxID=5854;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Simi
Matches 16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Howard R.F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NON_TER
NON_TER
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               09V7X3;
                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         325762;
                                                                                                                                                                                                                                                                                                                                                                                                                                  925762
                                                                                                                                                                                                                                                                                                                                                                                          RESULT 11
0.25762
AC 025762
DT 01-NOV
DT 01-NOV
DT 01-UNOV
DT 025762
DE STRAIN
RN NOD 1-IND
RN SEQUEN
RN HOWATC
RN HOW
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RC STRAIN-BERKELEY,

RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams W.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams W.D., Celniker S.E., Holt R.A.,

Ranarides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Ranarides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,

Ranarides P.G., Scherer S.E., Holder G., Naladon C.R., Miklos G.L.G.,

RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelsoon C.R., Miklos G.L.G.,

RA Marli J.F., Adbayani A., An H.J., Andrews Pfennkoch C., Baldwin D.,

Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

Ballew R.W., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,

RA Burtis K.C., Busam D.A., Buluck J., Brokstein P., Brottler P.,

Borkova D., Botchen M.R., Bouck J., Brokstein P., Brottler P.,

RA de Pablos B., Delcher A., Deng Z., Mays A.D., Duviov B.C., Dunn P.

A cherry J.M., Cawley S., Dahlke C., Rerriac C., Ferriac S., Fleischmann W.

RA de Pablos B., Delcher A., Howl Z., Gelpart W.M., Glasser K.,

RA Adrill M., Ralush F., Krapten G.H., Well M. H., Inbeywan C.,

RA Harris M.L., Barvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris M.L., Barvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Harris M.L., Barvey D., Helman T.J., Hernandez J.R., Howck J.,

RA Harris M.L., Barvey D., Hourn G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Alalali M., Kalush F., Krapten G.H., Ke Z., Kennison J.A., Ketchum K.A.,

Luu X., Mattei B., Modira C.D., Kraft C., Mravitz S., Mulp D., Lai Z.,

RA Markillow G., Milshian N.V., Mobarry C., Morris J., Puri V., Resse M.G.,

RA Merkulow G., Milshian N.V., Mobarry C., Morris J., Puri V., Rese M.G.,

RA Mount S.M., Woly M., Murphy B., Murphy L., Muzny D.M., McPhor D.R.,

RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,

RA Mang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbech J.,

RA Mang S.M., Woodage T., Worley K.C., Mu D., Yonk R.,

RA Gibbs R.N., Mejong F.W., Winder Z.,

RA Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               .;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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Best Local Similarity 76.9%; Pred. No. 14;
Matches 10; Conservative 1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PROSITE; PSO0094; CS_MTASE_1; UNKNOWN_1.
PROSITE; PSO0479; DAG_PE_BIND_DOM_1; 1.
PROSITE; PSO081; DAG_PE_BIND_DOM_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR001525; C5_DNA_meth. InterPro; IPR001219; DAG_PE-bind. InterPro; IPR001478; PDZ. InterPro; IPR001478; PE. InterPro; IPR000149; PH. InterPro; IPR000219; RhoGEF. Pfam; PF00130; DAG_PE-bind; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HSSP; Q12923; 3PDZ.
FlyBase; FBgn0023172; RhoGEF2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ffam; PF00621; RhoGEF; 1. SMART; SM0109; C1; 1. SMART; SM00228; PDZ; 1. SMART; SM00233; PH; 1. SMART; SM00325; RhoGEF; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3 PSSTKSSPSNVKS 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2559 AA;
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PROSITE; PS50106;
SEQUENCE 2559 AP
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Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Rujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
A Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
A cronin L.A., Shen M., Vanken S.E., Umayam L., Tallon L.J., Gill J.E.,
A dams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
Salzberg S.L., Fraser C.M., Venter J.C.;
N salzberg S.L., Fraser C.M., Venter J.C.;
REMBL, ARC1959; AAC39489.1;
REMBL, ARC19721; AAC39489.1;
REMBL, ARC19721; AAC3489.1;
REMBL, AC108721; AAC3489.1;
REMBL, AC108721; AAC3489.1;
REMSC, TOGA42:
REMSC, TOGA42:
READ ARCA C.M., PALCA COMMAN., PALCA COMMAN., PALCA C.M., PALCA C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spielmann T., Beck H.; "Analysis of stage specific transcription in Plasmodium falciparum reveals a set of genes exclusively transcribed in ring stage parasites."; Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases.
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01-007-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
HYPOTHETICAL 9.6 KDA PROTEIN (FRACHENT).
Plasmodium falciparum (isolate 3D7).
BURATYOCLA; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBL_TaxID=36329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   59.5%; Score 47; DB 5; Length 98; 62.5%; Pred. No. 2.4;
                                                                                                                                                                                                                                                                                                                                                                                                                                    328 AA; 35671 MW; B6B710475E34D08F CRC64;
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98 АА; 9590 МИ; ВС1857ЕВОD303042 СRC64;
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Llarity 64.7%; Pred. No. 4.8;
Conservative 2; Mismatches 4;
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3; Mismatches
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Job time: 212 sec
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PRINTS; PR00367; ETHRSPELEMNT.
ProDom; PD001423; AP2-domain;
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SPSSSSSSPSSSSSS 29
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Matches 11; Conserv
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Matches 10; Conserv
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Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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MEDLINE-98299844; PubMed-9634591;
Finkelstein R.R., Wang M.L., Lynch T.J., Rao S., Goodman H.M.;
The Arabidopsis abscisic acid response locus ABI4 encodes an APETALA
2 domain protein.";
Plant Cell 10:1043-1054(1998).
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MEDLINE-99225673; Pubmed-10207155;
Wang M.L., Belmonte S., Kim U., Dolan M., Morris J.W., Goodman H.M.;
"A cluster of ABA-regulated genes on Arabidopsis thaliana BAC
T07M07.";
                                                                                                                                                                                                                                                                                 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
STRAIN-CBAJ; TISSUE-BRAIN;
Ward-Bailey P.F., Johnson K.R.;
Ward-Bailey P.F., Johnson K.R.;
"Neuromuscular ataxia: a new spontaneous mutation in the mouse.";
Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
BRBL; AF232828; AAF35907.1; -.
MGD; MGI:104297; Noval.
InterPro; IPR000058; KH.
Pfam; PF00013; KH-domain; 3.
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Pred. No. 4.8;
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SEQUENCE 493 AA; 50302 MW; 7D09E8A55B0A7817 CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
AP2 DOMAIN FAMILY TRANSCRIPTION FACTOR HOMOLOG.
                                                                                                                                                            01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
VENTRAL NEURON-SPECIFIC PROTEIN 1 NOVA1 (FRAGMENT).
                                                                                                                       493 AA
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01-NOV-1998 (TrEMBLrel. 08, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last ann
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MEDLINE-20083487; PubMed-10617197;
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58.8%;
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         645 PSSTDNSPSNAKS 657
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Best Local Similarity
Matches 10; Conserv
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                                                                         RESULT 13
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HSV-2 strain SB5 C HSV-2 strain SB5 C Arabidopsis thalia Arabidopsis thalia

Title: Perfect score:

Sequence:

OM protein

Run on

Scoring table:

Searched:

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T-cell epitope; tetanus toxold; antigenic epitope; treatment; circumsporozoite protein; CSP; sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine;
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US DEPT HEALTH & HUMAN SERVICES.
                                                                                                             AAW56736
AAY44687
AAG05123
AAG50040
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AAB14870
AAY84335
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AAG38360
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 99WO-US18869
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                                                                                       Plasmodium falciparum
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WO200011179-A1.
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 AAY70299;
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 RESULT
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S. epidermidis ope
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Arabidopsis thalia
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Polypeptide antige
                                                                           Search time 66.28 Seconds (without alignments)
18.999 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                             **Sidestage **Side
                      Compugen Ltd
                                                                                                                                                                                                                             Total number of hits satisfying chosen parameters:
            GenCore version 4.5 Copyright (c) 1993 - 2000 Comp
                                                                                                                                                                                                         522463 seqs, 74073290 residues
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                                                                           January 29, 2002, 10:59:18
                                                                                                                                                                                                                                                                                     Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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AAG82568
AAB44822
AAB44823
AAB57133
AAG31170
AAG31170

    protein search, using sw model

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Gapop 10.0 , Gapext 0.5
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84
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Maximum DB seq length: 200000000
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The present sequence is the antigenic epitope P605, derived from the present sequence is the antigenic epitope P605, derived from the rhopery associated protein-1 (RAP-1) of the asexual blood stage of the separation of recombinant protein CpC/NIIMALVAC-1, which is a multivalent, multistage malarial protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial conformer. The recombinant protein comprises, melittin signal peptide, vaccine. The recombinant protein (CSP), sporozoite surface protein-2 from circumsporozoite protein (CSP), sporozoite surface protein-1 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (SSP-2), liver stage antigen-1 (LSA-1), merozoite surface protein-1 (ASP-1), malarial in an gamete antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen, Pfg27. These epitopes were obtained at different stages of the life cycle of P. falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting P. falciparum in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; r-cell epitope; tetanus toxoid; antigenic epitope; treatment; SSP-2; circumsporozoite protein; CSP; sporozoite surface protein-1; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated protein-1; RAP-1; gamete specific antigen; preyzo; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody;
Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
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23...50
7.label= Mature_CDC/NIIMALVAC-1
/note= "Recombinant multivalent malarial vaccine"
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/label= Melittin_signal_peptide
/note= "Derived from Honey bee"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 84; DB 21; 100.0%; Pred. No. 1.4e-07;
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Chimeric - Clostridium tetani.
Chimeric - Plasmodium falciparum.
                                                                                    Claim 2; Page 17; 52pp; English.
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Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                  17 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            19-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          02-MAR-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        honey bee
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAY70278;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Seguence
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The present sequence is that of recombinant protein CDC/NIIMALVAC-1, which is a multivalent, multistage malarial vaccine. The recombinant of protein comprises, melitin signal peptide, (His)6 tag, T-cell epitope protein comprises, melitin signal peptide, (His)6 tag, T-cell epitope content tetanus toxoid and 21 antigenic epitopes from circumsporzolte from tetanus toxoid and 21 antigenic epitopes from circumsporzolte content of protein (GSP), sporzolte surface protein (GSP-2), liver stage antigen-1 (LSA-1), merocolte surface protein 1 (MSP-1), MSP-2, apical membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), membrane antigen-1 (AMA-1), erythrocyte binding antigen-175 (EBA-175), rhoptry associated protein-1 (RAP-1) and gamete specific antigen Pfg27.

These epitopes were obtained at different stages of the life cycle of plasmodium falciparum. CDC/NIIMALVAC-1 vaccine has antiparasitic activity and can used for treatment and prevention of malarial infections. Anti-CDC/NIIMALVAC-1 antibodies can be used for detecting the content of the life cycle of protein in biological samples.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                        Novel recombinant protein as vaccine for treating malarial infection comprises antigenic peptides obtained from different stages of plasmodium falciparum life cycle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Antigenic polypeptide and DNA encoding it - having a determinant cross reactive with those on the rhostry organelles of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%; Score 84; DB 21; Length 350; 100.0%; Pred. No. 3.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Polypeptide antigenic to rhostry organelles of Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;
0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
      (NAIM-) NAT INST IMMUNOLOGY.
(USSH ) US DEPT HEALTH & HUMAN SERVICES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Malaria; vaccine; rhoptry organelles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAR06991 standard; protein; 782 AA.
                                                                                                                                                                                                Claim 3; Page 43-44; 52pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       89GB-0019064
89GB-0005857
                                                     Shi YP, Hasnain SE;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 LATRLMKKFKAEIRDFF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ridley RG, Scaife JG;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             plasmodium falciparum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1990-291721/39.
N-PSDB; AAQ06000.
                                                                                         WPI; 2000-237654/20.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              350 AA;
                                                                                                       N-PSDB; AAZ51336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            22-AUG-1989;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                                                            Lal AA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAR06991
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ANH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) via the production of vectors containing them which are used to produce hosts cells which express the oplypeptides. The polypeptides (II) fand/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their creatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent specifically claimed S. epidermidis genomic DNA polynucleotide sequences from the present invention. AAH55091 to AAH55091 to the avamalification of the present invention.
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N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification,
                                                                                                                                                                                                                                                       Gaps
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    S. epidermidis open reading frame protein sequence SEQ ID NO:2230.

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                                                                                     expression system using plasmid pMC9, and may then be used for immunisation against malaria. The product may also be used diagnostically to detect Abs directed against the parasite.
                                                                      Gene product may be isolated from a transformed E.coli (Y1088)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                                                                                                   Length 782;
                                                                                                                                                                                                                                                   Indels
merozoite form of the malaria parasite P falciparum.
                                                                                                                                                                                                                100.0%; Score 84; DB 11;
100.0%; Pred. No. 7.5e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 18; Page 597; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                               AAG82568 standard; Protein; 190 AA.
                                     Claim 1; Fig 2a-b; 29pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        09-NOV-2000; 2000WO-US30782.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0164258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis.
                                                                                                                                                                                                                                                                                                         03-SEP-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vaccination; endocarditis.
                                                                                                                                                                                                          Query Match
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                      1 LATRLMKKFKAEIRDFF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GLAX ) GLAXO GROUP LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2001-316495/33.
N-PSDB; AAH53418.
                                                                                                                                                            782 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Staphylococcus
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                                                                                                                                                             Seguence
                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG82568;
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AAH52304 to AAH53970 represent nucleic acids (I) encoding polypeptides (II), given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (II) given in AAG81454 to AAG83120, from Staphylococcus epidermidis. (I) and (II) can have antibacterial activity and therefore can be used in vaccination. The nucleic acids (I) may be used to produce the S. epidermidis polypeptides (II) wat the production of vectors containing them which are used to produce hosts cells which express the polypeptides. The polypeptides (II) (and/or nucleic acids) may then be used to vaccinate subjects and to raise antibodies against the bacteria. The polypeptides may also be used to assay for other inhibitors of their activity and therefore identify compounds that may be used for the treatment of S. epidermidis infections, e.g. endocarditis. AAH53971 to AAH55090 represent percent come the present invention. AAH55091 to AAH5509 represent oligonaciocide sequences and primers which are used
                                                                                                                                                                               ö
however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472, no sequences are present for SEQ ID NO:4455 to 4464.
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N.B. The present invention specifically claims all the polynucleotide sequences given in the sequence listing of the present specification, however the sequence listing only goes up to SEQ ID NO:4454 so even though sequences are given in the disclosure for SEQ ID NO:4465 to 4472,
                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nucleic acids encoding polypeptides from Staphylococcus epidermidis, useful for vaccinating against infections, e.g. endocarditis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               S. epidermidis open reading frame protein sequence SEQ ID NO:2906.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Staphylococcus epidermidis SR1 strain; infection; diagnosis;
                                                                                                                                      Length 190;
                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          no sequences are present for SEQ ID NO:4455 to 4464.
                                                                                                                                                                               5;
                                                                                                                                      53.6%; Score 45; DB 22; 52.9%; Pred. No. 5.3;
                                                                                                                                                         Pred. No. 5.3;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 18; Page 759; 2188pp; English.
                                                                                                                                                                                                                                                                                                                                                         AAG82906 standard; Protein; 1572 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      09-NOV-2000; 2000WO-US30782.
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120 lmtamikklkngikdff 136
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Staphylococcus epidermidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vaccination; endocarditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                  1 LATRLMKKFKAEIRDFF 17
                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1572 AA;
                                                                                                                                                      Best Local Similarity
Matches 9; Conserv
                                                                          190 AA;
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                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                AAG82906;
                                                                                                                                        Query Match
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The polynucleotide sequences given in AAC79799 to AAC79848 encode the human secreted proteins given in AAB44762 to AAB44811. AAB44812 to human secreted proteins sequences and proteins.

AAB44829 represent human secreted polypeptide sequences and proteins. CC homologous to them, which are used in the exemplification of the present invention. Human secreted proteins have activities based on the tissues invention. Human secreted proteins have activities are: consumptionally an ariarthritic; antirhematic; antirpoliferative; cytostatic; cardiant; vasortopic; antirhematic; antirpoliferative; cytostatic; cardiant; varioride; fungicide; and neuroprotective; antibaterial; virucide; fungicide; and cophthalmological. The polynucleotides and polypeptides can be used to ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, combits, notes, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a companied condition. Disorders which are diagnosed or treated include disorders, infections caused by bacteria, viruses and fungi and ocular disorders, infections caused by bacteria, viruses and fungi and ocular condition caused by bacteria, viruses and fungi and companied and ocular condition or supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The
                                                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative, cytostatic; cardiant; vasotropic; cerebroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; infection; hyperproliferative disorder; cardiovascular disorder; angiogenesis; cerebrovascular disorder; nervous system disorder; ocular disorder; wound healing; skin aging; food additive; preservative.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic'acid encoding human secreted proteins, used to treat, prevent, ameliorate or diagnose medical conditions such as cancer, and autoimmune diseases -
                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                     Gene 36 human secreted protein homologous amino acid sequence #121.
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0
    Length 1572;
                                                 5; Indels
            22;
        Score 45; DB 2
Pred. No. 48;
3; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Komatsoulis G;
                                                                                                                                                                                                                                    AAB44822 standard; Protein; 86 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (HUMA-) HUMAN GENOME SCI INC
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07-JAN-2000; 2000US-0174877.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-MAR-2000; 2000WO-US07726
            53.6%;
                                                                                                                                  1161 lmtamikklkngikdff 1177
                                                                                                                                                                                                                                                                                                                   (first entry)
Query Match
Best Local Similarity 52.5.
Conservative
                                                                                           1 LATRLMKKFKAEIRDFF 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Rosen CA, Ruben SM,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 2000-602355/57.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO200058336-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Homo sapiens.
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                                                                                                                                                                                                                                                                                                                       12-FEB-2001
                                                                                                                                                                                                                                                                                   AAB44822;
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                                                                                                                                                                                                                         AAB44822
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The polynucleotide sequences given in AAC79799 to AAC79848 encode the human secreted proteins given in AAB44762 to AAB44811. AAB44812 to AAB44829 represent human secreted polypeptide sequences and proteins concluded to the proteins are used in the exemplification of the present human secreted proteins have activities based on the tissues invention. Human secreted proteins have activities are:

and cells the genes are expressed in Examples of activities are:

inmunosuppressive; antiarthritic; antirhumatic; antiproliferative;

cytostatic; cardiant; vasotropic; cerebroprotective; nootropic;

cytostatic; cardiant; vasotropic; cerebroprotective; and polypeptides can be used to ophthalmological. The polynucleotides and polypeptides can be used to ophthalmological. The polynucleotides and polypeptides can be used to rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition or susceptibility to a pathological condition are diagnosed or treated include pathological condition are diagnosed or treated include autoimmune diseases, hyperproliferative disorders, cardiovascular
                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; infection; hyperproliferative disorder; cardiovascular disorder; angiogenesis; cerebrovascular disorder; nervous system disorder; ocular disorder; wound healing; skin aging; food additive; preservative.
polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC79790 to AAC79798 and AAB44761 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Nucleic acid encoding human secreted proteins, used to treat, prevent,
                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human secreted protein sequence encoded by gene 36 SEQ ID NO:122.
                                                                                                                                                                                            ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ameliorate or diagnose medical conditions such as cancer, and autoimmune diseases
                                                                                                                                                                                              4; Indels
                                                                                                                                                         DB 21;
                                                                                                                                                                                                  Mismatches
                                                                                                                                                           Score 43;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 381; 391pp; English.
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                                                                                                                                                                                                                                                                                                                                                                        AAB44823 standard; Protein; 86 AA.
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07-JAN-2000; 2000US-0174877.
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                                                                                                                                                             51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-FEB-2001 (first entry)
                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                      1 LATRLMKKFKAEIRD 15
                                                                                                                                                                                                                                                                           81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rosen CA, Ruben SM,
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67 latrflksfkanlen
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                                                                                                                                                                             Best_Local Similarity
Matches 8; Conserv
                                                                                                       86 AA;
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                                                                  invention.
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                   disorders, infections caused by bacteria, viruses and fungi and occular disorders. The polypeptides can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sumburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues and in chemotaxis. The polypeptides can also be used as a food additive or preservative to increase or decrease storage capabilities. AAC79790 to AAC79799 and AAB44761 represent sequences used in the exemplification of the present
                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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disorders, cerebrovascular disorders, angiogenesis, nervous system
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                                                                                                                                                                                                                                                                                                                                          DB 21; Length 86;
                                                                                                                                                                                                                                                                                                                                                                                         4; Indels
                                                                                                                                                                                                                                                                                                                                                                                         3; Mismatches
                                                                                                                                                                                                                                                                                                                                          51.2%; Score 43; 53.3%; Pred. No. 3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAB57133 standard; Protein; 98 AA.
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67 latrflksfkanlen 81
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Matches 8; Conserv
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                                                                                                                                                                                                                                                                  86 AA;
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                                                                                                                                                                                                                       invention.
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disorders such as neural, immune, muscular, reproductive, gastrointestinal, pulmonary, cardiovascular, renal, and proliferative disorders, wounds, and infectious diseases. AAF16506 to AAF16514 to AAB57303 represent sequences used in the exemplification of the present
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                                                                                                                                            Length 98;
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Pred. No. 5.7;
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53.3%;
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07-MAY-1999;
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                                                               invention.
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                                                                                               Sequence
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S-0136392 S-0137222 S-0137222 S-0137528 S-0137528 S-0138694 S-013884C S-013884C S-0138847 S-0138847 S-01398452	990S-0134455. 990S-0139456. 990S-0139458. 990S-0139458. 990S-0139461. 990S-0139462. 990S-0139462. 990S-0139750. 990S-0139750. 990S-0139750. 990S-0139899. 990S-0140891. 990S-0140891. 990S-0140891. 990S-0140991. 990S-0142803. 990S-0142803. 990S-0142803. 990S-0142803. 990S-0142803. 990S-0142977. 990S-0142977. 990S-0142977. 990S-0142977. 990S-0142977. 990S-0142977.	US-014432 US-014433 US-014433 US-014433 US-014438 US-01448 US-01448 US-01448 US-01450 US-0145
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                                            Gaps
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                  Score 43; DB 21; Length 297;
Pred. No. 18;
4; Mismatches 1; Indels
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                                                                                                                                   AAG31170 standard; Protein; 335 AA.
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990S-0126264
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99US-0137502.
99US-0137724.
99US-0138094.
                    Query Match
Best Local Similarity 58.3%;
Matches 7; Conservative
 99US-0162142
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36 ldkfksdigdff 47
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Score 43; DB 21; Length 335;
Pred. No. 21;
4; Mismatches 1; Indels
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Best Local Similarity 58.3%;
Matches 7; Conservative '
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99US-0151930.
99US-0152363.
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99US-0158029.
99US-0158232.
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26-0CT-1999;
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05-OCT-1999;
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                                                                                                                                                                                             7-AUG-1999;
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07-OCT-1
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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9905-0136021
9905-0136021
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99US-0138847.
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99US-0139454.
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99US-0123548.
99US-0125788.
99US-0126264.
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99US-0138094
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                                             (first entry)
                                                                                                           Arabidopsis thaliana.
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07-MAY-1999;
11-MAY-1999;
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20-MAY-1999;
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07-JUN-1999;
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                             AAG31169;
RESULT 11
        AAG31169
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AAG04103
ID AAG04103 standard; Protein; 186 AA.
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58.3%;
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92 ldkfksdigdff 103
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Matches
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Gaps

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Length 353; Indels

DB 21;

Score 43; DB: Pred. No. 22; 4; Mismatches

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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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04 - JUN - 1999;
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Pred. No. 16;
1; Mismatches 3; Indels
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69.2%;
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99US-0161406
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 50.0
Best Local Similarity 69.2
Matches 9; Conservative
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| 10 lmkkvqgeirdrf 22
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36-Aug-1999;
37-Aug-1999;
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9US-0140695 9US-0140695 9US-0140692 9US-0141287 9US-0141287 9US-0142184 9US-0142184 9US-0142180 9US-0142803 9US-0142803 9US-014384 9US-014384 9US-0144865	9905 - 01444986 9905 - 01444331 9905 - 0144331 9905 - 0144334 9905 - 0144335 9905 - 0144884 9905 - 0144884 9905 - 0145989 9905 - 0145989 9905 - 0145989 9905 - 0145989 9905 - 0145989 9905 - 0145989 9905 - 0145989	9905-0146389 9908-0147038 9908-0147302 9908-0147302 9908-0147302 9908-0147416 9908-0147416 9908-0147416 9908-0148171 9908-014864 9908-014864 9908-014864 9908-014864 9908-014902 9908-014992 9908-014992 9908-014992 9908-014992 9908-014992 9908-014992 9908-016986 9908-016986 9908-016986 9908-016986 9908-016986	007-010-006
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.
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Pred. No. 18;
1; Mismatches
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990S-0161363. 48.8%; 50.0%; Query Match 48.8 Best Local Similarity 50.0 Matches 8; Conservative LATRLMKKFKAEIRDF 16 06-0CT-1999) 07-0CT-1999) 12-0CT-1999; 13-0CT-1999; 13-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 14-0CT-1999; 12-0CT-1999; 21-0CT-1999; 21-0CT-1999; 22-0CT-1999; 22-0CT-1999; 23-0CT-1999; 25-0CT-1999; 26-0CT-1999; 26-0CT-1999; 26-0CT-1999; 28-0CT-1999; 28-0CT-1999; 28-0CT-1999; 28-0CT-1999; 28-0CT-1999; П à pp

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Search completed: January 29, 2002, 10:59:19 Job time: 2243 sec

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Sequence 150 Sequence 57, Sequence 150 Sequence 1 Sequence 5

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METHODS AND AN ACETYL COA CARBOXYLASE GENE
FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN
OIL CONTENT OF PLANTS
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TITLE OF INVENTION: METHODS AND AN ACETYL CON CONTROL OF TITLE OF INVENTION: FOR CONFERRING HERBICIDE TOLERANCE AND ITTLE OF INVENTION: OIL CONTENT OF PLANTS
NUMBER OF SEQUENCES: 11
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/417,089
INFORMATION FOR SED ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 amino acids
TYPE: amino acids
TYPE: amino acids
TYPE: anino acids
TYPE: Amino acids
TYPE: AMINEDNESS: Single
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Pred. No. 1.1e+02;
3; Mismatches 4; Indels
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US-08-311-611A-150
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US-08-372-105-57
US-08-306-473A-150
US-08-209-762-57
US-08-621-803-47
US-08-621-803-45
US-08-119-263-150
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US-08-657-162-57
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Patent No. 6069298
GENERAL INFORMATION:
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Best Local Similarity 53.3
Matches 8; Conservative
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MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                  Search time 32.24 Seconds
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/cgn2_6/ptodata/2/laa/5B_COMB.pep:*
/cgn2_6/ptodata/2/laa/AA_COMB.pep:*
/cgn2_6/ptodata/2/laa/AB_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
/cgn2_6/ptodata/2/laa/PCTUS_COMB.pep:*
                                              GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-08-417-089-6
US-08-695-551-6
US-08-695-551-6
US-08-695-421-6
US-08-695-421-6
US-08-603-133B-15
US-08-470-260-5
US-08-471-491-5
US-08-477-451-2
US-08-477-451-2
US-08-477-451-2
US-08-477-451-2
US-08-717-312-2
US-08-717-312-2
US-08-717-312-2
US-08-717-313-18
US-08-266-408-2
US-08-266-408-2
US-08-266-408-2
US-08-266-408-2
US-08-266-408-2
US-08-269-437-2
US-08-053-614-4
US-08-316-397B-4
US-08-316-397B-4
US-08-316-397B-4
US-08-316-397B-4
US-09-259-437-4
US-09-259-437-4
US-09-259-437-4
US-09-253-614-4
US-09-259-437-4
US-09-253-63-64
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                                                                                                                                                                                                                                                                  January 29, 2002, 10:59:57
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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                                                                                                                                                                                                                                                                                                                                                                                                            US-09-763-397A-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq length: 0 seq length: 2000000000
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Match Length
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Maximum DB
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Gaps

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13-APR-1998
13-APR-1998
18: 800
18: 800
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Somers, D. A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM Compatible OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO: 6
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-FEB-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 48.8
Best Local Similarity 53.3
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |||||| : |:|: |
919 LATRLPRNLKSELED 933
                                                                                                                                                                                                                                                                                                                                              single
                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE: protein HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 LATRLMKKFKAEIRD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE: 05-FEB APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE: 05-APR APPLICATION NUMBER:
                                APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                  TYFE: SIRSTRANDEDNESS: SIR
                                                                                                                                                                                                                                                                                                                            amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                FILING DATE: 13 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             FRAGMENT TYPE: P. ORIGINAL SOURCE: US-08-930-285-6
                                                                                                                                                                                                                                                                                                                                                                                                                 2
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE:
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Sequence 6. Application US/08930285
Patent No. 6222099
GENERAL INFORMATION:
APPLICANT: Regents of the University of Minnesota, et al.
TITLE OF INFORMINGENIC PLANTS EXPRESSING ACETYL COA CARBOXXLASE GE NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;
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Pred. No. 1.1e+02;
3; Mismatches 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ALUNESSEE: Schwegman, Lundberg, Woessner & Kluth, P. A. STREET: P. O. Box 2938
CITY: Minneapolis
STATE: MN
                                  Lundberg, Woessner & Kluth, P.A.
                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/695,651
FILING DATE: 12-AUG-1996
CLASSIPECATION: 435
CLASSIPECATION: 435
PROOR APPLICATION: DATE:
APPLICATION NUMBER: 08/417089
FILING DATE: 05-AFR-1995
APPLICATION NUMBER: 08/014326
FILING DATE: 05-FEB-1993
APPLICATION NUMBER: 07/917462
FILING DATE: 31-701-1993
APPLICATION NUMBER: 07/9138674
FILING DATE: 18-JUN-1990
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERNCE/DOCKET NUMBER: 600.318US3
TELECOMMINICATION:
TELEPHONE: 612-373-6900
                                                                                                                   ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPACTED
OPERATING SYSTEM: DOS
SOFTWARE: FASTENCY OF SOFTWARE
APPLICATION DUMBER: US/08/695,65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY 2.02
ZIP: 55402
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
Authorither: IBM Compatible
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SEQUENCE CHARACTERISTICS:
LENGTH: 2325 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; MOLECULE TYPE: protein
; FRAGMENT TYPE: N-terminal
US-08-695-651-6
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                                3: Schwegman,
P.O. Box 2938
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LATRLMKKFKAEIRD 15
                                              STREET: P.O. COTTY: Minneapolis
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SOFTWARE: FastSEQ
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Best Local Similarity
Matches 8; Conserv
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                                                                                                      USA
                                   ADDRESSEE:
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US-08-930-285-6
                                                                                                      COUNTRY:
                                                                                    STATE:
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APPLICANT: Somers, D. A.
APPLICANT: Wyse, D. L.
APPLICANT: Wyse, D. L.
APPLICANT: Egil, M. A.
APPLICANT: Egil, M. A.
APPLICANT: Lutz, S. M.
APPLICANT: Lutz, S. M.
TITLE OF INVENTION: METHODS AND AN ACETYL COA CARBOXYLASE GENE
TITLE OF INVENTION: FOR CONFERRING HERBICIDE TOLERANCE AND AN ALTERATION IN OIL
NUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 41; DB 4; 1
Pred. No. 1.1e+02;
3; Mismatches 4;
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SOFTWARE: FASTSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/695,421
FILING DATE: 23-AUG-1996
CLASSIFICATION: 800
PRIOR APPLICATION:
                                                                                                          NAME: Embretson, Janet E.
REGISTRATION NUMBER: 39,665
REFERENCE/DOCKET NUMBER: 600.318US4
TELECOMMUNICATION INFORMATION:
TELEPHONE: 612-339-0331
TELEFAX: 612-339-3061
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/04625
FILING DATE: 04-APR-1996
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                               GENERAL INPORMATION:
APPLICANT: Redmond, Mark J.
APPLICANT: Redmond, Mark J.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
STATE: CA
COUNTRY: USA
IP: 94025
COMPUTER: READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Tab PC-Compatible
COMPUTER: Pacentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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o
                                                            Score 40; DB 1; Length 775;
Pred. No. 55;
3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47.6%; Score 40; DB 1; Length 775; 70.0%; Pred. No. 55; 0; Indels Live 3; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  33,208
ER: 9313-0004.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PELICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTOMEY/GENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.0C
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-7250
METELE COMMUNICATION INFORMATION:
TELEPHONE: (415) 327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-08-470-260-5
Sequence 5, Application US/08470260
Patent No. 6077706
GENERAL INFORMATION:
APPLICANT: COVACCI, Antonello
APPLICANT: Bugnoli, Massimo
                                                                                                                                                                                                                                                                                             Sequence 16, Application US/07603133B Patent No. 5298244
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: (412,
TELEFAX: 706141
INFORMATION FOR SEQ ID NO: 16:
SEQUENCE CHARACTERISTICS:
LENGTH: 775 amino acids
""R: AMINO ACID
                                                                47.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 47.6
Best Local Similarity 70.0
Matches 7; Conservative
                                                            Query Match
Best Local Similarity 70.0
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: unknown
MOLECULE TYPE: protein
US-07-603-1338-16
                                                                                                                                            1 LATRLMKKFK 10
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543 MATKVMKKFK 552
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543 MATKVMKKFK 552
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US-07-603-133B-16
      US-07-603-133B-15
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0
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Patent No. 5298244
GENERAL INFORMATION:
APPLICANT: Redmond, Mark J.
APPLICANT: 19az, Mohammed K.
APPLICANT: Parker, Michael D.
TITLE OF INVENTION: ASSEMBLED VIRAL PARTICLES AND THEIR
TITLE OF INVENTION: USE IN A VACCINE TO ROTAVIRAL DISEASE
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 2325;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 41; DB 4; Length 232
Pred. No. 1.1e+02;
3; Mismatches 4; Indels
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/603,133B
FILING DATE: 19901025
CLASSIFICATION: 424
ATTONNEY/AGENT INFORMATION:
NAME: ROBINS, Roberta L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9313-0004.00
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRAX: (415) 327-2250
TELEFRAX: (415) 327-2951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Morrison & Foerster
STREET: 545 Middlefield Road, Suite 200
CITY: Menlo Park
                                                                               NAME: Woessner, Warren D
REGISTRATION NUMBER: 30,440
REFERNCE/DOCKET NUMBER: 600.318US2
TELECOMMUNICATION:
TELEPHONE: 612-373-6900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94025
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                   APPLICATION NUMBER: 07/538674
FILING DATE: 18-JUN-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                            INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 2325 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: (415) 327-2951
TELEX: 706141
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERESTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 53.3%;
Matches 8; Conservative
APPLICATION NUMBER: 07/55
FILING DATE: 18-JUN-1990
                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: protein FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 775 amino acids
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unknown
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                                                                                                                                                                                       TELEFAX: 612-339-3061
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LATRLMKKFKAEIRD 15
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Gaps

us-09-763-397a-23.rai

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RESULT 9
US-00-466-662-5
US-00-466-662-5
; Sequence 5, Application US/08466662B
; Patent No. 613063
; GEKERAL INFORMATION:
; APPLICANT: Covacci, Antonello
; APPLICANT: Telford, John
; APPLICANT: Rappuoli, Raino
; APPLICANT: Rappuoli, Raino
; TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
; TITLE OF INVENTION: Diagnostics
; TITLE REPERBNCE: CHIROD57
; CURRENT FILING DATE: 1995-06-06
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
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                                    Length 1147;
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Pred. No. 1,2e+02;
5; Mismatches 4; Indels
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US-08-477-451-2
Sequence 2, Application US/08477451
Sequence 2, Application US/08477451
Patent No. 529865
GENERAL INFORMATION:
APPLICANT: COVACCI, Antonello
TITLE OF INVENTION: Helicobacter Pylori Cagi Region
NUMBER OF SEQUENCES: 46
CORRESPONDENCE ADDRESS:
ADDRESSEE: CAlron Corporation
STREET: Emeryville
CITY: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,451
                                    Score 39; DB 3; ]
Pred. No. 1.2e+02;
5; Mismatches 4
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07-JUN-1995
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CLASSIFTCATION: 435
ATORNEY AGENT INFORMATION:
NAME: McClung, Barbara G.
REGLSTRATION NUMBER: 33,113
REFERENCE/DCOKET NUMBER: 0335.002
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIF: 94608-298
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/WS-DOS
                                      46.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; TYPE: PRT; ORGANISM: Helicobacter pylori
US-08-466-662-5
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Best Local Similarity 43.87
Fig. Conservative
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                                    Query Match
Best Local Similarity 43.8
Matches 7; Conservative
                                                                                                                       1 LATRLMKKFKAEIRDF 16
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Patent No. 6090611
GRMERAL INFORMATION:
APPLICANT: Covacci, Antonello
APPLICANT: Happioli, Massimo
APPLICANT: Happioli, Massimo
APPLICANT: Happioli, Massimo
APPLICANT: Macchia, Giovanni
APPLICANT: Macchia, Giovanni
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful For Vaccines And
TITLE OF INVENTION: Diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
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Pred. No. 1.2e+02;
5; Mismatches 4; Indels
         APFLICANT: Macchia, Giovanni
APPLICANT: Rappuoli, Rino
TITLE OF INVENTION: Helicobacter Pylori Proteins Useful
TITLE OF INVENTION: for Vaccines and Diagnostics
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSE: Chiron Corporation
ADDRESSE: Chiron Street
                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/470,260
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CURRENT APPLICATION NUMBER: US/08/471,491B
CURRENT FILING DATE: 1995-06-06
NUMBER OF SEQ ID NOS: 8
SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: McClung, Barbara G.
REGISTRATION NUMBER: 33.13.3
REFERENCE/DOCKET NUMBER: 0316.001
TELECOMMUNICATION INCREATION:
TELEPHONE: ($10) 651-3342
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1147 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/256,848
FILING DATE: 21-0CT-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                         ZIP: 94608-2916
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
Telford, John
Macchia, Giovanni
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; ORGANISM: Helicobacter pylori
US-08-471-491-5
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Best Local Similarity 43.0%
Pest Local 7; Conservative
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| 413 LSEKEKEKFRTEIKDF 428
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                                                                                                                                                                                  Emeryville
California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                linear
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                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE
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US-08-471-491-5
                                                                                                                                                                                                                         COUNTRY:
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Query Match
Best Local Similarity
Matches 5; Conserva
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Baum, James A.
TITLE OF INVENTION: Bacillus thuringiensis Transposon Tn5401
TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
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Pred. No. 3.3e+02;
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Pred. No. 68;
8; Mismatches 3; Indels
                                                                                                                                                                                                                                                                        4; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. ADDRESSEE: Nadel STREET: 1601 Market Street, 36th Floor CITY: Philadelphia STATE: Pennsylvania COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/089,986
FILING DATE: 19930708
                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/08089986
Patent No. 5441884
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: EGOLf, Christopher
REGISTRATION NUMBER: 27633
REFRENCE/CDCKET NUMBER: 7205
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.08;
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
TELEPHONE: 510-601-2708
TELEPAX: 510-655-3542
INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                46.48;
                                                                        LENGTH: 3289 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                |: : :||: ||:||
1944 LSEKEKEKFRTEIKDF 1959
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                                                                                                                                                                                                                              Query Match
Best Local Similarity 43.8
Matches 7; Conservative
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28 LHTKTLKEYTSDLKDF 43
                                                                                                                                    ; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-477-451-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ; MOLECULE TYPE: protein US-08-089-986-2
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY:
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US-08-089-986-2
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RESULT

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Sequence 2, Application US/08478585
Patent No. 5650308
GENERAL INFORMATION:
APPLICANT: Baum, James A.
TITLE OF INVENTION: Bacillus thuringiensis Transposon Tn5401
TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS: ADDRESS: ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/O A.S.
ADDRESSEE: Nadel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:

APPLICANT: Baum, James A.

APPLICANT: Baum, James A.

TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Panitch Schwarze Jacobs & Nadel c/o A.S. Nadel

STREET: 1601 Market Street, 36th Floor
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ed. No. 68;
Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/478,585 FILING DATE: 07-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                             STREET: 1601 Market Street, 36th Floor CITY: Philadelphia STATE: Pensylvania COUNTRY: U.S.A. ZIP: 19103
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,986
FILING DATE: 08-010-1993
ATTORNEY/AGENT INFORMATION:
NAME: Egolf, Christopher
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2, Application US/08717312
Patent No. 5776449
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 72
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-757-1590
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Egolf, Christopher REGISTRATION NUMBER: 27633
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  : 306 amino acids
amino acid
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28 LHTKTLKEYTSDLKDF 43
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: 1601 Market
CITY: Philadelphia
STATE: Pennsylvania
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28 LHTKTLKEYTSDLKDF 43

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APPLICAMY: Baum, James A.
APPLICAMY: Baum, James A.
TITLE OF INVENTION: Bacillus thuringiensis Transposon Tn5401
TITLE OF INVENTION: and Its Use in a Site-Specific Recombination System For TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development TITLE OF INVENTION: Recombinant Bacillus thuringiensis Strain Development MUNDRES OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
ADDRESSEE: Panitch Schwarze Jacobs & Nadel C/O A.S. Nadel
STREET: 1601 Market Street, 36th Floor
CITY: Philadelphia
STREET: ATTE: Pennsylvania
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOPTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/07886
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 5;
68;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pred. No. 68;
8; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Search completed: January 29, 2002, 10:59:58
Job time: 2144 sec
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 37;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: US 08/089,986
FILING DATE: 08-UUL-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                       STATE: Pennsylvania
COUNTRY: U.S.A.
2 IP: 19103
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: OF SYSTEM: PC-DOS/MS-DOS
                                                           RESULT 15
PCT-0594-07886-2
PCT-0594-07886-2
Sequence 2, Application PC/TUS9407886
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity 31.2%;
Matches 5; Conservative
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amino acid
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28 LHTKTLKEYTSDLKDF 43
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 37; DB 1; Length 306; Pred. No. 68;
OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/717,312 FILING DATE: 20-SEP-1996 CLASSIFICATION: 435 PRIOR APPLICATION DATA: APPLICATION NUMBER: 08/266,408 FILING DATE: 24-JUL-1994 FILING DATE: 08-JUL-1994 APPLICATION NUMBER: US 08/089,986 FILING DATE: 08-JUL-1993 INFORMATION FOR SEQ ID NO: 2: SEQUENCE CHARRATERISTICS: SEQU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/266,408
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Pred. No. 68;
8; Mismatches
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/089,986
FILING DATE: 08-010-1993
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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31.2%;
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Best Local Similarity 31.2
Matches 5; Conservative
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28 LHTKTLKEYTSDLKDF 43
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CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                     linear
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US-08-266-408-2
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GenCore version 4.5

Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: January 29, 2002, 11:00:39; Search time 34.94 Seconds

(without alignments)
37.063 Million cell updates/sec

Title: US-09-763-397A-23

Perfect score: 84
Sequence: 1 LATRLMKKFKAEIRDFF 17

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5
```

Total number of hits satisfying chosen parameters: 219241 Minimum DB seq length: 0

219241 seqs, 76174552 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 200000000 Post-processing: Minimium Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_68:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

S	Description	rhoptry-associated	tRNA pseudouridine	SRG1 protein-relat	photosystem I chai	tryptophantRNA 1	hypothetical prote	hypothetical prote	4	hypothetical prote	probable annexin [probable cytochrom	threonyl-tRNA synt	DNA-directed RNA p	acetyl-CoA carboxy	acetyl-CoA carboxy	acetyl-CoA carboxy	probable binding p	homolog		hypothetical prote	cytochrome p450 -	cytochrome P450 -	DNA polymerase - p	outer layer protei	outer layer protei		probable chloropla	prolipoprotein dia	hypothetical prote
SUMMARIES	ID	S27833	B82902	T05552	A32124	S73894	F85056	B71135	T52255	C86168	н84808	T52172	D69318	S01393	T02921	T02750	T02235	H83478	686305	T05551	н85230	T03246	T03260	S51275	VPXRWT	VPXRW7	VPXRW9	D84542	F71712	C70388
	DB	7	7	7	7	7	7	7	7	~	7	7	~	• •	~	~	~	~	~	7	7	7	7	7	Н	٦		~	7	7
	Length	782	227	353	141	346	398	456	496	743	319	503	619	1530	1625	1685	2325	302	346	326	527	535	535	268	774	775	176	1206	268	344
de	Query Match	100.0	51.2	51.2	20.0	20.0	20.0	20.0	20.0	50.0	٠.	ъ.		8		ъ.	•		7.	•	٠	•		•	٠			47.6	46.4	46.4
	Score	84	43	43	42	42	42	42	42	42	41	41	41	41	41	41	41	40	40	40	40	40	40	40	40	40	40	40	39	39
	Result No.	П	7	Э	4	S	9	7	œ	6	10	11	12	13	14	15	16	17	18	19	20	21	22	23	24	22	56	27	28	53

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0; Gaps

Score 43; DB 2; Length 227; Pred. No. 11; 3; Mismatches 4; Indels

Query Match 51.2%; Best Local Similarity 56.2%; Matches 9; Conservative

SRG1 protein - Ara	glutamate dehydrog	2-dehydro-3-deoxyp	nitrogen regulatio	outer capsid prote	HsdRl protein - My	cytotoxin-associat	genome polyprotein	conserved hypothet	hypothetical prote	hypothetical prote	translation elonga	hypothetical prote	cystathionine gamm	2-dehydro-3-deoxyp	probable DNA-direc
S44261	G84176	S40411	G71666	A48480	549394	B48281	A44059	A83362	E86127	T06720	JH0416	F64456	A35016	S40412	S41618
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358	429	511	601	176	986	1215	2105	230	235	337	397	398	509	541	547
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46	46	46	46	46	46	46	46	45	45	45	45	45	45	45	45
39	39	33	39	39	39	39	39	38	38	38	38	38	38	38	38

ALIGNMENTS

RESULT 1 S27833 Indeptry-associated protein 1 precursor - malaria parasite (Plasmodium falciparum) N.Alternate names: protective antigen C.Species: Plasmodium falciparum C.Species: Paramodium falciparum C.Species: Paramodium C.Species: Nacession: A45514; S77833 R.Ridley, R.G.; Takacs, B.; Lahm, H.W.; Delves, C.J.; Goman, M.; Certa, U.; Matile, H Mol. Blochem. Parasition, and sequence of a protective rhoptry antigen from Plasmodiu A; Reference number: A45514; MUID:90348711 A; Accession: A45514 A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-782 <ri2> A; Cross-references: GB:M32853; NID:9160656; PID:9160657 C; Superfamily: Plasmodium falciparum rhoptry-associated protein 1</ri2>
Query Match Best Local Similarity 100.0%; Pred. No. 8e-06; Matches 17; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 LATRLMKKFKAEIRDFF 17
RESULT 2 B83902 tRNA pseudouridine 55 synthase UU354 [imported] - Ureaplasma urealyticum C; Species: Ureaplasma urealyticum C; Species: Ureaplasma urealyticum C; Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000 C; Accession: B82902 R; Class, J.I.; Lefkowitz, E.J.; Glass, J.S.; Heiner, C.R.; Chen, E.Y.; Cassell, G.H. submitted to GenBank, February 2000 A; Bescription: The complete sequence of Ureaplasma urealyticum: Alternate views of a A; Reference number: A82870 A; Reference number: A82870 A; Status: preliminary A; Molecule type: DNA A; Kesidues: 1-27 < CLAL> A; Cross-references: GB:AE002132; GB:AF222894; NID:g6899327; PIDN:AAF30763.1; GSPDB:GN A; Experimental source: serovar 3; biovar 1 C; Genetics: A; Gene: truB; UU354 A; Genetic code: SGC3

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Gaps

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Indels

Length 141;

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Nighteridate Hames: Imported to the control of the 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                tryptophan--tRNA ligase (EC 6.1.1.2) trpS - Mycoplasma pneumoniae (strain ATCC 29342)
N;Alternate names: hypothetical protein A65_orf346; tryptophanyl-tRNA synthetase trpS
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A;Cross-references: GB:NC_001268; NID:97267205; PIDN:CAB77916.1; GSPDB:GN00140
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Pred. No. 25;
3; Mismatches
                                                                                                                                      Score 42; DB 2
Pred. No. 11;
4; Mismatches
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C; Superfamily: photosystem I chain II
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Best Local Similarity 57.1%;
Matches 8; Conservative
                                                                                                                                           50.0%;
50.0%;
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165 ATRLFKKLRVEIEMF 179
                                                                                                                                           Query Match 50.0
Best Local Similarity 50.0
Matches 8; Conservative
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| 165 LAQRIQKKFKLKLR 178
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                                                                                                                                                                                                                                                                                                                                                                                              68 LGTQLRTKFKPKIQDY
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Matches 9; Conserv
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N;Alternate names: photosystem I reaction center chain II
S;Species: Synechocystis sp.
A;Variety: PCC 6803
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Jun-2000
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Jun-2000
C;Date: 07-Jun-1990 #sequence_revision 07-Jun-1990 #text_change 20-Jun-2000
B;Reilly, P.; Hulmes, J.D.; Pan, Y.C.E.; Nelson, N.
J. Biol. Chem. 263, 17658-17662, 1988
A;Title: Molecular cloning and sequencing of the psaD gene encoding subunit II of photos
A;Reference number: A92692; MUID:89034300
A;Accession: A32124
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A; Residues: 1-141 <KAN>
A; Cross-references: EMBL:D90899; GB:AB001339; NID:g1651650; PIDN:BAA16688.1; PID:g165176
A; Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
A; Note: the nucleotide sequence, P: Rigoni, F:; de Martini, E:; Giacometti, G.M.
Eur. J Blochem. 234, 459-465, 1995
A; Title: Fujment' Protein complexes from the photosynthetic membrane of the cyanobacteriu A; Reference number: S67978; MUID:96128174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:J04195; NID:g154480; PIDN:AAA88625.1; PID:g154481
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda
DNA Res. 3, 109-136, 1996
A;Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
                                                                                                                                                                                                                                                                                                                                                                SRG1 protein-related protein F24A6.150 - Arabidopsis thaliana C; Species: Arabidopsis thaliana (mouse-ear cress) C; Species: Arabidopsis thaliana (mouse-ear cress) C; Date: 23.Apr-1999 #sequence_revision 23.Apr-1999 #text_change 23.Jul-1999 C; Accession: T05552 R; Bevan, M.; Wedler, H.; Wedler, E.; Wambutt, R.; Hoheisel, J.; Mewes, H.W.; Mayer, K.F. submitted to the Protein Sequence Database, February 1999 A; Accession: T05552 A; Accession: T05552
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A; Residues: 1-353 <BEV>
A; Cross-references: EMBL:AL035396
A; Experimental source: cultivar Columbia; BAC clone F24A6
C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Introns: 84/3; 164/2; 273/3
A;Note: F24A6.150
C;Superfamily: 1-aminocyclopropane-1-carboxylate oxidase
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18;
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Pred. No.
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A; Residues: 2,'S',4-9,'L',11-13 <BAR>
C; Genetics:
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143 IAPRLVKIFKYQIMDF 158
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92 LDKFKSDIQDFF 103
                                                           LATRLMKKFKAEIRDF
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Best Local Similarity
'-hag 7; Conservē
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A; Residues: 1-141 <REI>
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Length 398;

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Nature 408, 816-820, 2000
A; Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Liu, J.H.; Li, Y.; Lin, X; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A; Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A; Tille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A; Reference number: A66141; MUID:21016719
A; Reference rickels
A; Molecule type: DNA
A; Residues: 1-743 <STO>
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C:Species: Arabidopsis thallana (mouse-ear cress)
C:Date: 200-Ct-2000 #sequence_revision 20-Oct-2000 #text_change 16-Feb-2001
C:Accession: T5172; E84633
R:Mizutani, M.; Ward, E.; Ohta, D.
Plant Mol. Biol. 37, 39-52, 1998
A;Title: Cytochrome p450 superfamily in Arabidopsis thallana: isolation of CDNAs, dif
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Species: Arabidopsis thaliana Gnouse-ear cress)
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
C; Accession: H84808
C; Accession: H84808
M; Kaul, S; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tailon, euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter Nature 402, 761-768, 1999
A; Tille: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A; Reference number: A84420; MuID:20083487
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R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujil, C.Y
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C; Genetics:
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A; Cross-references: GB: AE002093; NID: 93785997; PIDN: AAC67343.1; GSPDB: GN00139
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52;
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Pred. No. 34;
2; Mismatches
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Pred. No. 52;
1; Mismatches
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Best Local Similarity 61.5%;
Matches 8; Conservative
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Best Local Similarity
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A;Map position: 2
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C;Species: 1752255
R;Udvardl, M.K.; Metzger, J.D.; Krishnapillai, V.; Peacock, W.J.; Dennis, E.S.
R;Udvardl, M.K.; Metzger, J.D.; Krishnapillai, V.; Peacock, W.J.; Dennis, E.S.
R;Udvardl, M.K.; Metzger, J.D.; Krishnapillai, V.; Peacock, W.J.; Dennis, E.S.
R;Tile: Cloning and nucleotide sequence of a full-length cDNA from Thlaspi arvense that A;Reference number: 226005
A;Reference number: 226005
A;Reference number: 226005
A;Residues: 1-496 <UDV>
A;Residues: 1-49
                                                                                                                             hypothetical protein PH0846 - Pyrococcus horikoshii
C;Species: Pyrococcus horikoshii
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Date: 14-Aug-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: B71135
B;Kawarabayasi, Y: Sawada, M: Horikawa, H.; Haikawa, Y.; Hino, Y.; Yamamoto, S.; Sekin
M: Ohfuku, Y: Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Oguchi
DNA Res. 5, 55-76, 1998
A.Title: Complete sequence and gene organization of the genome of a hyper-thermophilic a
A.Reference number: A71000; MUID:98344137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A; Cross-references: GB: AP0000003; NID: 93236130; PIDN: BAA29940.1; PID: 93257257
A; Experimental source: strain OT3
A; Experimental source: strain OT3
A; Note: this accession replaces an interim accession for a sequence replaced by GenBank C; Genetics:
A; Gene: PH0846
C; Superfamily: Methanobacterium thermoautotrophicum conserved hypothetical protein MTH19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           hypothetical protein [imported] - Arabidopsis thaliana C:Species: Arabidopsis thaliana (mouse-ear cress) C:Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001 C:Accession: C86168 A:Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.
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Pred. No. 35;
3; Mismatches
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66.78;
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Best Local Similarity 66.7
Matches 8; Conservative
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318 RVMKKLQAEIRE 329
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35 TRLLKEFSKDKRTFF
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Best Local Similarity
Matches 8; Conserv
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C;Superfamily: yeast DNA-directed RNA polymerase III 160K chain
C;Keywords: DNA binding; nucleotidyltransferase; nucleus; transcription; zinc finger
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Local Similarity 53.3%;
les 8; Conservative
                                                                                                   48.8%;
                                                                                                     Query Match 48.8
Best Local Similarity 63.6
Matches 7; Conservative
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220 LATRLPRNLKSELED 234
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A; Residues: 1-1685 <ASH>
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Matches
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M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, leuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
A.Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DNA-directed RNA polymerase (EC 2.7.7.6) III 170K chain - Trypanosoma brucei brucei C; Species: 10.86p-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999 R; Rocek, J.; Evers, R.; Cornelissen, A.W.C.A.
Nucleic Acids Res. 16, 8753-8772, 1988
A.Title: Structure and sequence of the gene for the largest subunit of trypanosomal BA.Reference number: $01393 MUID:89016560
A.Reference number: $01393 MUID:89016560
A.Residues: 1-1530 < KOE>
A.Residues: 1-1530 < KOE>
A.Residues: 1-1530 < KOE>
A.Cross-references: EMBL:X12494; NID:910523; PIDN:CAA31014.1; PID:910524
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                                                                                                                                                 A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-503 <STO>
A;Cross-references: GB:AE002093; NID:g4115378; PIDN:AAD03379.1; GSPDB:GN00139
C;Genetics:
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C;Superfamily: human cytochrome P450 CYP2D6; cytochrome P450 homology
C;Keywords: heme: iron; metalloprotein
F;304-468/Domain: cytochrome P450 homology <P45>
F;446/Binding site: heme iron (Cys) (axial ligand) #status predicted
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Pred. No. 64;
5; Mismatches
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Pred. No. 52;
3; Mismatches
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Best Local Similarity 66.7%;
Matches 8; Conservative
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Matches 7; Conservative
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AVKLLKQLEAELSDF 102
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RVMKKVQAEIRE 339
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A; Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA A; Pathway: fatty acid biosynthesis
A; Note: biotin cofactor
C; Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biot C; Keywords: ligase
F; 127-199/Domain: lipoyl/biotin-binding homology < LPB>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Description: catalyzes the ATP-dependent carboxylation of acetyl-CoA to malonyl-CoA C; Superfamily: human acetyl-CoA carboxylase; biotin carboxylase homology; lipoyl/biot C; Keywords: ligase F; 68-140/Domain: lipoyl/biotin-binding homology CLPB>
                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: T02921
R;Ashton, A.R.; Jenkins, C.L.D.; Whitfeld, P.R.
Plant Mol. Biol. 24, 35-49, 1994
A;Title: Molecular cloning of two different cDNAs for maize acetyl CoA carboxylase.
A;Reference number: S42659; MUID:94154242
A;Accession: T02921
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translated from GB/EMBL/DDBJ
A; Molecule type: mRNA
A; Residues: 1-1625 <ASH>
A; Cross-references: EMBL:224449; NID:g1272684; PIDN:CAA80822.1; PID:g1272685
A; Experimental source: strain B73; leaf
C; Function:
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C;Species: Zea mays (maize)
C;Spate: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 21-Jan-2000
C;Accession: T02750
R;Ashton, A.R.
Ashton, A.R.
A;Reference number: 214716
A;Reference number: 214716
A;Accession: T02750
                                                                                                                                                                                                                                                                                                                           acetyl-CoA carboxylase (EC 6.4.1.2) (clone A3) - maize (fragment)
C;Species: Zea mays (maize)
C;Date: 24-Mar_1999 #sequence_revision 24-Mar-1999 #text_change 21-Jul-2000
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Length 1530;
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Best Local Similarity 53.3%; Pred. No. 1.7e+02;
Matches 8; Conservative 3; Mismatches 4.
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Pred. No. 1.6e+02;
3; Mismatches 4;
Score 41; DB 1; 1
Pred. No. 1.5e+02;
3; Mismatches 1;
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human rotav simian 11 r caenorhabdi

P26451 Q06895 P17464 P24348 P95064 P53910 P52199

human

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5'-PHOSPHATE + H(2)O.
-1- SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PSI GC LOOP OF TRANSFER RNAS (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                     20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last nunotation update)
TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55
SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Glass J.I., Lefkowitz E.J., Glass J.S., Heiner C.R., Chen E.Y., Cassell G.H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          urealyticum.";
Nature 407:757-762(2000).
-!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITION 55 IN THE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ureaplasma parvum (Ureaplasma urealyticum biotype 1).
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
Mycoplasmataceae; Ureaplasma.
NCBI_TaxID=134821;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "The complete sequence of the mucosal pathogen Ureaplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Lyase; tRNA processing; Complete proteome.
SEQUENCE 227 AA; 25765 MW; FA1CADC357D6AD36 CRC64;
                                                                                                                                                                                                                                                                                                                       227 AA
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               VP4_ROTHY
VP4_ROTSS
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RHOE_HUMAN
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Copyright (c) 1993 - 2000 Compugen Ltd.
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the European Bloinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Aral B., Benelli C., Ait-Ghezala G., Amessou M., Fouque F., Maunoury C., Creau W., Kamoun P., Marsac C.; "Mutations in PDX1, the human lipoyl-containing component X of the pyruvate dehydrogenase-complex gene on chromosome llp1, in congenital
                                                                                                                                                                                                                                                                                                                                                                pyruvate
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Ling M., McEachern G., Seyda A., Mackay N., Scherer S.W.,
Ling M., McEachern G., Seyda A., Mackay N., Scherer S.W.,
Bratinova S., Beatty B., Glovannucci-Dzielli M.L., Robinson B.H.;
"Detection of a homozygous four base pair deletion in the protein X
gene in a case of pyruvate dehydrogenase complex deficiency.";
Hum. Mol. Genet. 7:501-505(1998).
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                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDILINE-97930399; PubMed=9242632;
MEDILINE-97930399; PubMed=9242632;
Harris R.A., Bowker-Kinley M.M., Wu P., Jeng J., Popov K.M.;
"Dihydrolipoamide dehydrogenase-binding protein of the human pyruvat dehydrogenase complex. DNA-derived amino acid sequence, expression, and reconstitution of the pyruvate dehydrogenase complex.";
J. Biol. Chem. 272:19746-19751(1997).
                                                                                                  PYRUVATE DEHYDROGENASE PROTEIN X COMPONENT, MITOCHONDRIAL PRECURSOR (DIHYDROLIPOAMIDE DEHYDROGENASE-BINDING PROTEIN OF PYRUVATE
                                                                                                                                                                                                         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-97264341; PubMed-9110174; Yu W., Andersson B., Worley K.C., Muzny D.M., Ding Y., Liu W., Ricafrente J.Y., Wentland M.A., Lennon G., Gibbs R.A.; "Large-scale concatenation cDNA sequencing.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -1- SUBCELLULAR LOCATION: MITOCHONDRIAL MATRIX.
-1- DISEASE: DEFECTS IN PDX1 ARE A CAUGS OF LACTICACIDEMIA.
-1- SIMILARIY: BELONGS TO THE 2-OXOACID DEHYDROGENASE FAMILY.
-1- SIMILARIY: COUNTAINS 1 LIPOXL-BINDING DOMAIN.
                                                                                                                                                 DEHYDROGENASE COMPLEX) (E3-BINDING PROTEIN) (E3BP) (PROX).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          the Swiss Institute of Bioinformatics and the
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Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
               000330; 099783; 060221;
15-UUL-1999 (Rel. 38, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
  Α
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MEDLINE=98153629; PubMed=9399911;
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  STANDARD;
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    ODPX_HUMAN
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--- FUNCTION: PSAD CAN FORM COMPLEXES WITH FERREDOXIN AND FERREDOXIN---- OXIDOREDUCTASE IN PHOTOSYSTEM I (PS 1) REACTION CENTRE.
--- SUBDNIT: PS I FROM SYNECHOCYSTIS SP. CONTAINS SEVEN DIFFERENT POLLYPEPTIDES. THE POLYPEPTIDE CORRESPONDING TO SUBUNIT II FROM HIGHER PLANTS IS MISSING.
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MEDLINE-89034300; PubMed-3141423;
Realily P., Hulmes J.D., Pan Y.-C.E., Nelson N.;
Molecular cloning and sequencing of the psab gene encoding subunit
II of photosystem I from the cyanobacterium, Synechocystis sp. PCC
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01-FEB-1991 (Rel. 17, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PHOTOSYSTEM I REACTION CENTRE SUBUNIT II (PHOTOSYSTEM I 16 KDA
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PYRUVATE DEHYDROGENASE PROTEIN
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LIPOYL (BY SIMILARITY).
R -> C (IN REF. 1).
A -> R (IN REF. 3).
A -> S (IN REF. 3).
A -> S (IN REF. 1 AND 2).
W; 9CFOCIDAE9E12EF9 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales; Synechocystis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   140 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                Pfam; PF00189; 2-oxoacid_dh; 1.
Pfam; PF00189; 2-oxoacid_dh; 1.
PRINTS; PR01217; PRICHEXTENSN.
ProDom; PD001115; 20xoacid_dh; 1.
PROSITE; PS00189; LIPOYL; 1.
Transit peptide; Mitcofondrion; Lipoyl.
TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biol. Chem. 263:17658-17662(1988).
                                                                                                                                                                                          Interpro; IPR000089; Biotin_lipoyl.
Interpro; IPR003016; Lipoyl.
Interpro; IPR002965; P_rich_extensn.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                InterPro; IPR001078; 20xoacid_dh
                    Y13145; CAA73606.1; -.
U82328; AAC39661.1; -.
AL138810; CAC12641.1; -.
U79296; AAB50223.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97 LJ
23 R
41 A
251 A
54122 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    51.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA Res. 3:109-136(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      482 LATRFLKSFKANLEN 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 LATRLMKKFKAEIRD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                              53
501
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         POLYPEPTIDE) (PSI-D).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       251
501 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID-1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PSAD OR SLR0737
                                                                                                                                     MIM; 245349;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             .;
8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PSAD_SYNY3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BINDING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P19569;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KESULT 3
PSAD_SYNY3
                                                                                                          EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CHAIN
                                                                                EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           6803.
                                                        EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         op ′
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Gaps

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INIT_MET SEQUENCE

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Thlaspl.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'Cloning and sequencing of a full-length cDNA from Thlaspi arvense L.
    Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Udvardi M.K., Metzger J.D., Krishnapillai V., Peacock W.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 496;
                                                                                                                                                                      Length 346;
                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
                                          "HIGH" REGION.
"KMSKS" REGION.
ATP (BY SIMILARITY).
66CF4FFCCE9C2F95 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      that encodes a cytochrome P-450.";
Plant Physiol. 105:755-756(1994).
-:- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           136 HEME (BY SIMILARITY).
56387 MW; 59D3A6B34F6685D8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
CYTOCHROME P450 71B1 (EC 1.14...) (CYPLXXIB1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.0%; Score 42; DB 1; 66.7%; Pred. No. 12;
                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                           496 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       503 AA.
                                                                                                                                                                                            Pred. No. 8.4;
                                                                                                                                                                                                                  3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                      50.0%; Score 42; 57.1%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR001128; Cyt_P450.
Pfam; PF00065; p450; 1.
PRO14TS; PR00463; EP4501.
PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oxidoreductase; Monooxygenase; Heme.
BINDING 436 436 HEME (B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                             PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Thlaspi arvense (Field pennycress)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
TISSUE-Shoot apex;
MEDLINE-94345014; PubMed-8066138;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3;
                                                                                                          39079 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L24438; AAA19701.1;
                                                                                                                                                                                            Best Local Similarity 57.1
Matches 8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                             STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STANDARD;
                                                                                                                                                                                                                                                                                     || |: |||| ::|
165 LAQRIQKKFKLKLR 178
                                                                                                                                                                                                                                                          1 LATRLMKKFKAEIR 14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1:111 :1111: .
318 RVMKKLQAEIRE 329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 RLMKKFKAEIRD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
8; Conserv?
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 496 AA;
                                                                                                          346 AA;
                            Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Dennis E.S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C726_ARATH
O65787;
                                                                                                                                                                                                                                                                                                                                                                                                           THLAR
                                                                                      BINDING
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CYP71B1.
                                                                                                                                                                                                                                                                                                                                                                                                           C7B1_THL
P49264;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BINDING
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C726_ARATH
                                                                                                                                                                                                                                                                                                                                                                   RESULT 5
C7B1_THLAR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A D
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                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@lib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Herrmann R.; "Complete sequence analysis of the genome of the bacterium Mycoplasma
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  -i- CATALYTIC ACTIVITY: ATP + L-TRYPTOPHAN + TRNA(TRP) = AMP + PYROPHOSPHATE + L-TRYPTOPHANYL-TRNA(TRP).
-i- SUBUNIT: HOMODIMER (BY SIMILARITY).
-i- SUBCELLULAR LOCATION: CYTOPLASMIC.
-i- SIMILARITY: BELONGS TO CLASS-I AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
03-NGS-2001 (Rel. 40, Last annotation update)
TRYPTOPHANYL-TRNA SYNTHETASE (EC 6.1.1.2) (TRYPTOPHAN--TRNA LIGASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mycoplasma pneumoniae.
Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Himmelreich R., Hilbert H., Plagens H., Pirkl E., Li B.-C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4; Indels
                                                                                                                                                                                                                                                                                                                                                                 263C35D5B47B9F8E CRC64;
                                                                                                                                                                                                                                                                                                                    Photosynthesis; Photosystem I; Complete proteome. INIT_MET 0 \ 0
                                                                                                                                                                                                                                                                                                                                                                                                                               Score 42; DB 1;
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE000056; AAB96216.1; -.
InterPro; IPR002305; tRNA-synt_1b.
InterPro; IPR001412; tRNA-synt_1.
InterPro; IPR002306; tRNA-synt_trp.
InterPro; IPR002306; tRNA-synt_trp.
PRINTS; PR01039; TRNASYNTHTRP.
PROSITE; PS00178; AA_TRNA_LIGASE_I; FALSE_NEG.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      346 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4; Mismatches
-! - SIMILARITY: BELONGS TO THE PSAD FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Š
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic Acids Res. 24:4420-4449(1996)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            [1]
SEQUENCE FROM N.A.
STRAIN-ATCC 29342 / M129;
MEDLINE-97105885; PubMed-8948633;
                                                                                                                                                                                                                                                                                                                                                              140 AA; 15513 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mycoplasmataceae; Mycoplasma.
                                                                                                                                                                                                            EMBL; J04195; AAA88625.1; -. EMBL; D90899; BAA16688.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                             50.0%;
                                                                                                                                                                                                                                                      PIR; A32124; A32124.
InterPro; IPR003685; PsaD.
Pfam; PF02531; PsaD; 1.
                                                                                                                                                                                                                                                                                                                                                                                                      Ouery Match
Best Local Similarity 50...
8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 LATRLMKKFKAEIRDF 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LGTQLRTKFKPKIQDY 82
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TRPS OR MPN265 OR MP568.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               pneumoniae."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SYW_MYCPN P75510;
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Gaps

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                                                                                                                                                                                                                        Klenk H.-P., Clayton R.A., Tomb J.-F., White O., Nelson K.E., Ketchum K.A., Dodson R.J., Gwinn M., Hickey E.K., Peterson J.D., Richardson D.L., Kerlavage A.R., Graham D.E., Kyrpides N.C., Fleischmann R.D., Quackenbush J. Lee N.H., Sutton G.G., Gill S., Kirkness E.F., Dougherty B.A., McKenney K., Adams M.D., Loftus B., Peterson S., Reich C.I., McNeil L.K., Badger J.H., Glodek A., Zhou L., Overbeek R., Gocayne J.D., Weidman J.F., McDonald L., Utterback T., Sadow P.W., D'Andrea K.P., Bowman C., Fujil C., Garland S.A., Mason T.M., Olsen G.J., Fraser C.M., Smith H.O., Woese C.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Interpro; IPR002106; AA_tRNA_ligase_II.
Interpro; IPR002310; tRNA-synt_2b.
Interpro; IPR002320; tRNA-synt_2b.
Interpro; IPR002320; tRNA-synt_thr.
Pfam; PF00587; tRNA-synt_Thr.
PROJITE; PS00179; AA_TRNA_LIGASE_II_1; 1.
PROSITE; PS00339; AA_TRNA_LIGASE_II_2; FALSE_NEG.
Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -!- SIMILARITY: BELONGS TO CLASS-II AMINOACYL-TRNA SYNTHETASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         "The complete genome sequence of the hyperthermophilic, sulphate-reducing archaeon Archaeoglobus fulgidus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
ZINC (CATALYTIC) (BY SIMILARITY).
839AB5DZBES45A02 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1988 (Rel. 09, Created)
01-NOV-1988 (Rel. 09, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
DNA-DIRECTED RNA POLYMERASE III LARGEST SUBUNIT (EC 2.7.7.6).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -i - CATALYTIC ACTIVITY: ATP + L.THREONINE + TRNA(THR) = AMP
PYROPHOSPHATE + L.THREONLY.TRNA(THR).
-i - COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
-i - SUBCELLUIAR LOCATION: CYTOPLASMIC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 48.8%; Score 41; DB 1; Length 619;
                                                       Archaea; Euryarchãeota; Archaeoglobales; Archaeoglobaceae;
Archaeoglobus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT; 1530 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ed. No. 22;
Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CATALYTIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pred. No.
                                                                                                                                                                                   STRAIN=VC-16 / DSM 4304 / ATCC 49558;
MEDLINE-98049343; PubMed-9389475;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; AE001066; AAB90685.1; -.
TIGR; AF0548; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               72150 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            46.78;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ouery Match
Best Local Similarity 46...
T; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 390:364-370(1997).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           288
340
                                                Archaeoglobus fulgidus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | :|:|: ||: ||
88 AVKLLKQLEAELSDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              196 4
196 2
288 2
340 3
464 4
619 AA;
                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                    NCBI_TaxID=2234;
                        THRS OR AF0548
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RPC1_TRYBB
P08968;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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    This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstationthe European Bioinformatics Institute. There are no restrictions on its most by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                             core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
TRANSMEM 10 30 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-CV. COLUMBIA;
MEDLINE-20083487; PubMed-10617197;
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
Eujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
Moffat K.S., Cronin L.A., Shen M., Vanaken S.E., Umayam L.,
Tallon L.J., Gill J.E., Adams M.D., Carrera A.J., Creasy T.H.,
Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=CV. COLUMBIA: TISSUE=Seedling;
MEDLINE=9881573;
Mizutani M., Ward E., Ohta D.;
"Cytochrome P450 superfamily in Arabidopsis thaliana: isolation of CDNAs, differential expression, and RFLP mapping of multiple
                                                                                                                                               Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Sequence and analysis of chromosome 2 of the plant Arabidopsis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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15-JUL-1998 (Rel. 36, Last sequence update)
20-MG-2001 (Rel. 40, Last annotation update)
THREONYL-TRNA SYNTHETASE (EC 6.1.1.3) (THREONINE--TRNA LIGASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1; Length 503;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402:761-768(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HEME (BY SIMILARITY).
71AFAD5370AEDFF6 CRC64;
                                                                                                               Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core evencsids II; Brasslcales; Brasslcaceae; Arabidopsis.
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYPCHROME P450 7186 (EC 1.14.-.)
CYP71B6 OR AT2G24180 OR F27D4.9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 41; DB
Pred. No. 18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AC005967; AA003379.1; -.
InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; P450. 1.
PROWINS; PR00463; EP4501.
PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRT;
                                                                                                                                                                                                                                                                                                                                                                                                       cytochromes P450.";
Plant Mol. Biol. 37:39-52(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  503 AA; 57008 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; D78604; BAA28536.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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328 RVMKKVQAEIRE 339
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                           eurosids II; Bra
NCBI_TaxID=3702;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Venter J.C.
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SYT_ARCFU RESULT

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Caenorhabditis elegans.
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                                                     NCBI_TaxID=6239;
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Q9LTL0;
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                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=90036885; PubMed=2808366;
Smith J.L., Levin J.R., Agabian N.;
"Molecular characterization of the Trypanosoma brucei RNA polymerase I and III largest subunit genes.";
J. Biol. Chem. 264:18091-18099(1989).
-: FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
                                                                                                                                                                                                                                                                                                                                             -1- SUBCELLULAR LOCATION: NUCLEAR.
-1- MISCELLANBOUS: THREE DISTINCT ZINC-CONTAINING RNA POLYMERASES ARE FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE RIBOSOMAL RNA FOUND IN EUKARYOTIC NUCLEI: POLYMERASE I FOR THE PL
                                                                                                                                                                                                                                                                                                       -1- SUBUNIT: RNA POLYMERASE III CONSISTS OF ABOUT 15 DIFFERENT SUBUNITS. THIS SUBUNIT IS THE LARGEST COMPONENT OF RNA POLYMERASE
                                                                                                                                                                                                                                                                               -! - CATALYTIC ACTIVITY: N NUCLEOSIDE TRIPHOSPHATE - N PYROPHOSPHATE +
               Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                    PRECURSOR, POLYMERASE II FOR THE MRNA PRECURSOR, AND POLYMERASE III FOR 5S AND TRNA GENES.

-!- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              YMP9_CAEEL STANDARD; PRT; 194 AA.
Q10952;
O1-OCT-1996 (Rel. 34, Last sequence update)
O1-OCT-2001 (Rel. 40, Last annotation update)
HYPOTHETICAL 22.0 KDA PROTEIN B0361.9 IN CHROMOSOME III PRECURSOR.
                                                                                                                                                                                                                                                OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS SUBSTRATES.
                                                SEAURINGE FROM N.A.
STRAIN=427 / ISOLATE MITAT 1.2A;
MEDLINE=89016560; Pubmed=3174432;
Cornelissen A.W.C.A., Evers R., Koeck J.;
"Structure and sequence of the gene for the largest subunit of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pfam; PF00623; RNA_pol_A; I.
Pfam; PF01854; RNA_pol_A2; I.
Transferase; DNA-directed RNA polymerase; Transcription; Zinc; Zinc-finger; Vuclear Protein.
Zinc-finger; Vuclear B7 C3H-TYPE (POTENTIAL).
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0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   D -> E (IN REF. 2).
I -> V (IN REF. 2).
MW; FC03D700CEF9D742 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              3; Mismatches
                                                                                                                      trypanosomal RNA polymerase III.";
Nucleic Acids Res. 16:8753-8772(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            EMBL; X12494; CAA31014.1; -.
EMBL; M27163; AAA30233.1; -.
PIR; S01393; S01393.
InterPro; IPR000722; RNA_pol_A.
InterPro; IPR002879; RNA_pol_A2.
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Trypanosoma brucei brucei
Eukaryota; Euglenozoa; Ki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7; Conservative
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1035 RKFKDDIQDFF 1045
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE
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YMP9_CAEEL
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MEDLINE-20277480; Pubmed-10819329;
Sato S., Nakamura Y., Kaneko T., Katoh T., Asamizu E., Tabata S.;
Sato S., Nakamura Y., Kaneko T., Katoh T., Sequence "Structural analysis of Abidopsis thaliana chromosome 3. I. Sequence features of the regions of 4,504,864 bp covered by sixty Pl and TAC
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edons; core eudicots; Rosidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POTENTIAL.
HYPOTHETICAL PROTEIN B0361.9.
; 79C9F7A2570AAF38 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 194;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                          Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases.
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DNA Res. 7:131-135(2000).
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; eudicotyledons; core e eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   47.6%; Score 40; DB 1; 42.9%; Pred. No. 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20-AUG-2001 (Rel. 40, Created)
20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
CYTOCHROME P450 71B26 (EC I.14...).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embry
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      6; Mismatches
   Eukaryota; Metazoa; Nematoda; Chromadorea
Rhabditidae; Peloderinae; Caenorhabditis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; U00031; AAK18868.1; -... WormPep; B0361.9; CE00838.
InterPro; IPR003014; PAN.
InterPro; IPR003609; Pan_app.
Pfam; PF00024; PAN; 1.
SMART; SM00473; PAN_AP; 1.
Hypothetical protein; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 22017 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  170 SKLMKKLSAKVKEF 183
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity
                                                                                                                                    SEQUENCE FROM N.A. STRAIN-BRISTOL N2;
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351 RVMKKLQAEVRAY 363

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VP4_ROTHT
P11200;
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
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                                                                                                                Oxidoreductase; Monooxygenase; Transmembrane; Heme; Multigene family.
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                                                                                                                                                                                                                                              DB 1; Length 500;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=CV. CI31A;
MEDLINE=95124291; PubMed=7823905;
Frey M., Kliem R., Saedler H., Gierl A.;
"Expression of a cytochrome P450 gene family in maize.";
MOI. Gen. Genet. 246:100-109(1995).
                                                                                                                                                                                                                                                                                         1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gierl A.;
Submitted (MAR-1997) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE CYTOCHROME P450 FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            475 HEME (BY SIMILARITY).
60715 MW; F92A696108E2ADAF CRC64;
                                                                                                                                POTENTIAL.
HEME (BY SIMILARITY).
7 7BD8352058F4C52C CRC64;
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TRANSMEM 23 43 POTENTIAL.
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28;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C7C3_MAIZE STANDARD; PRT; 535 AA. P93703, Q43256; Created) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last sequence update) 15-DEC-1998 (Rel. 37, Last annotation update) CXTOCHROME P450 71C3 (EC 1.14.--).
                                                                                                                                                                                                                                              47.6%; Score 40; DB 66.7%; Pred. No. 27; ative 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 40;
Pred. No. 2
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EMBL; X11403; CAA72207.1; -.
INLECTPO; IPRO11128; CYL_P450.
PÉm; PPO0067; p450; 1.
PROSITE; PS00086; CYTOCHROME_P450; 1.
EMBL; AB024038; BAB02452.1; -.
InterPro; IPR001128; Cyt_P450.
Pfam; PF00067; P450; 1.
PRINTS; PR00385; P450.
PROSITE; PS00086; CYTOCHROME_P450; 1.
                                                                                                                                                                              57080 MW;
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Best Local Similarity 53.8
Matches 7; Conservative
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322 RVMKKVQAEIRN 333
                                                                                                                                                                                                                                                                                                                                     4 RLMKKFKAEIRD 15
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Best Local Similarity
Matches 8; Conserv
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C7C3_MAIZE
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Gaps
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01-NOV-1990 (Rel. 16, Last sequence update)
02-NOC-2001 (Rel. 40, Last annotation update)
00TER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4)
(CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC...) (POTENTIAL).
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MEDLINE-88275070; PubMed-2839714;
Gorziglia M., Green K., Nishikawa K., Taniguchi K., Jones R.,
Kapikian A.Z., Chanock R.M.;
Kapikian A.Z., Chanock R.W.;
Sequence of the fourth gene of human rotaviruses recovered from asymptomatic or symptomatic infections.";
J. Virol. 62:2978-2984(1988).
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D397E5C6125A8FA8 CRC64;
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OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP5.
                                                                                                                                                          strain St. Thomas 3).
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                                                                                                                                                        Human rotavirus (serotype 4 / strain St. Thome
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10960;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VP4_ROTHM STANDARD; PRT; 775 AA P11197; 01-JUL-1989 (Rel. 11, Created) 01-JUN-1990 (Rel. 16, Last sequence update)
774 AA
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InterPro; IPR000416; Cap_VP4.
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Best Local Similarity 70.0°
  STANDARD;
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Gorziglia M., Hoshino Y., Buckler-White A., Blumentals I., Glass R., Flores J., Kapikian A., Chanock R.M.;
"Conservation of amino acid sequence of VPB and cleavage region of 84-kba outer capsid protein among rotaviruses recovered from asymptomatic neonatal infection.";
Proc. Natl. Acad. Sci. U.S.A. 83:7039-7043(1986).
-!- SUBCELLULAR LOCATION: OUTER CAPSID.
-!- PTM: VPB IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE OTHER PRODUCT IS VP5.
-!- SIMILARITY: BELONGS TO THE ROTAVIRUS VP4 PROTEIN FAMILY.
PIR; E28839; VPXRW7.
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111199; (Rel. 11, Created)
01-VUL-1989 (Rel. 16, Last sequence update)
01-NOV-1990 (Rel. 16, Last annotation update)
02-NGG-2001 (Rel. 140, Last annotation update)
02-ORG-2001 (Rel. 140, Last annotation update)
(CONTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4)
20-AUG-2001 (Rel. 40, Last annotation update)
OUTER CAPSID PROTEIN VP4 (HEMAGGLUTININ) (OUTER LAYER PROTEIN VP4)
[CONTAINS: OUTER CAPSID PROTEINS VP5 AND VP8].
                                                                                                    Gorziglia M., Green K., Nishikawa K., Taniguchi K., Jones R., Kapikian A.Z., Chanock R.M.; Sequence of the fourth gene of human rotaviruses recovered from asymptomatic or symptomatic infections."; J. Virol. 62:2978-2984(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                 (POTENTIAL).
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Pred. No. 42;
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                                         Human rotavirus (serotype 1 / strain M37).
Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10954;
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Viruses; dsRNA viruses; Reoviridae; Rotavirus.
NCBI_TaxID=10955;
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N-LINKED
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                                                                                  SEQUENCE FROM N.A.
MEDLINE-88275070; PubMed-2839714;
                                                                                                                                                                                                                                                                                                    PIK; EZB839; VPXRW7.
InterPro; IPR000416; Cap_VP4.
Pfam; PF00426; VP4; 1.
Coat protein; Glycoprotein.
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543 MATKVMKKFK 552
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775 AA;
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MEDLINE=86313706; PubMed=3018754;
MEDLINE=86313706; PubMed=3018754;
Gorziglia M., Hoshino Y., Buckler-White A., Blumentals I., Glass R.,
Flores J., Kapiklan A.Z., Chancok R.M.;
"Conservation of amino acid sequence of vp8 and cleavage region of
84-kba outer capsid protein among rotaviruses recovered from
asymptomatic neonatal infection.";
Proc. Natl. Acad. Sci. U.S.A. 83:7039-7043(1986).
-!- SUBCELLIARA LOCATION: OUTER CAPSID.
-!- PTM: VP8 IS ONE OF TWO TRYPSIN CLEAVAGE PRODUCTS OF VP4; THE
OTHER PRODUCT IS VP5.
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STRAIN=MADRID E;
MEDLINE=99039499; Pubmed=9823893;
Andersson S.G.E., Zomorodipour A., Andersson J.O.,
Sicheritz-Ponten T., Alsmark U.C.M., Podowski R.M., Naeslund A.K.,
Eriksson A.-S., Winkler H.H., Kurland C.G.;
"The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N-LINKED (GLCNAC...) (POTENTIAL).
SEQUENCE FROM N.A.

MEDLINE-88275070; PubMed=2839714;
Gorziglia M., Green K., Nishikawa K., Taniguchi K., Jones R.,
Kapikian A.Z., Chanock R.M.;
Kapikian A.Z., Chanock R.M.;
Sequence of the fourth gene of human rotaviruses recovered from asymptomatic or symptomatic infections.";
J. Virol. 62:2978-2984(1988).
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PIR; G28839; VPXRW9.
PIR; G25904; VPXRMN.
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Rickettsiaceae; Rickettsieae; Rickettsia.
NCBL_TaxID=782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 776;
42;
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30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PROLIPOPROTEIN DIACYLGLYCERYL TRANSFERASE (EC 2.4.99.-).
LGT OR RP046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRC64;
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OUTER CAPSID PROTEIN VP8.
OUTER CAPSID PROTEIN VP5.
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Matches 7; Conservative
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This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation-the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities againes a license greement (See http://www.isb-sib.ch/announce/or send an email to license@lsb-sib.ch).
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            Nature 396:133-140(1998).
-!- FUNCTION: TRANSFERS THE N-ACYL DIGLYCERIDE GROUP ON WHAT WILL BECOME THE N-TERMINAL CYSTEINE OF MEMBRANE LIPOPROTEINS
                                                               (BY SIMILARITY).
--- PATHWAY: FIRST STEP IN LIPOPROTEINS BIOSYNTHESIS.
---- SUBCELLULAR LOCATION: INTEGRAL MEMBRANE PROTEIN (POTENTIAL).
---- SIMILARITY: BELONGS TO THE LGT FAMILY.
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46.4%; Score 39; DB 1; Length 268;
Best Local Similarity 58.3%; Pred. No. 20;
Matches 7; Conservative 4; Mismatches 1; Indels
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InterPro; IPROJ1640; LGT.
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TRANSEM 18 38 POTIT TRANSMEM 64 84 POTIT
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Search completed: January 29, 2002, 11:16:19 Job time: 148 sec

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us-09-763-397a-23.rspt

Title: Perfect score:

Sequence:

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Run on:

Scoring table:

Searched:

Minimum DB Maximum DB

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Q95hg1 arabidopsis
Q95up2 arabidopsis
Q95up2 arabidopsis
Q95up2 arabidopsis
Q76308 trichomonas
Q0627 trichomonas
Q964y3 tetrahymena
Q61712 caenorhabdi
Q96201 human rotav
Q86221 rotavirus s
Q86221 rotavirus s
Q86221 rotavirus s
Q86211 buman rotav
Q90314 human rotav
Q90315 human rotav
Q951f3 arabidopsis
Q92hf5 streptococc
Q92u08 arabidopsis
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 Q9zvj6 arabidopsis
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Mol. Biochem. Parasitol. 51:327-330(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN=INDJ-1 (CLONE 1 OF INDIAN ISOLATE J);
BEDLINES-08519224, PUDNEd-8784775;
HOWART R.F., Peterson C.;
"Limited RAP-1 sequence diversity in field isolates of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
STRAIN INDJ-1 RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5833;
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153 Aa; 18273 MW; 6AA7AC2C4AAC447C CRC64;
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Best Local Similarity 100.0%; Pred. No. 4.1e-06;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN=INDJ-1 (CLONE 1 OF INDIAN ISOLATE J);
MEDLINE-92244303; Pubmed-1574089;
                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 AA
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Mol. Biochem. Parasitol. 77:95-98(1996)
EMBL; U41075; AAC47091.1;
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SEQUENCE FROM N.A.
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025730 plasmodium
025875 plasmodium
026007 plasmodium
09431 plasmodium
094420 plasmodium
094429 plasmodium
09444 plasmodium
091422 plasmodium
091423 arabidopsis
095932 arabidopsis
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O58576 pyrococcus
Q65856 beet yellow
Q9zwa0 arabidopsis
Q9nkn3 leishmania
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Q25764 plasmodium
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- 2000 Compugen Ltd.
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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5: sp_invertebrate:*
6: sp_mammal:*
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Score

Result Š 5 6 8 8 110 111 113 114 116 118 118

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EMBL; U41073; AAC47089.1; -. NON_TER 1 1 1 1 SMON_TER 163 163 SEQUENCE 163 AA; 19522 MW
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Matches 17; Conservative
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Best Local Similarity 100.
Matches 17; Conservative
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Submitted (FEB-1995) to
EMBL; U20985; AAA63681.1
SEQUENCE 782 AA; 9002
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                                                                                                                                                                                                                 "The sequence of the p82 rhoptry protein is highly conserved between two Plasmodium falciparum isolates.";
MOI. Biochem. Parasitol. 51:327-330(1992).
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SCHUENCE FROM N.A.
STRAIN=INDC (INDIAN ISOLATE C);
MEDLINE=96379224; PubMed=8784775;
Howard R.F., Peterson C.;
"Limited RAP-1 sequence diversity in field isolates of Plasmodium falciparum.";
MOI. Biochem. Parasitol. 77:95-98(1996).
EMBL; U41077; AAC47093.1;
                                                                                                                                                                                                                                                                                                    Howard R.F., Peterson C., "Limited RAP-1 sequence diversity in field isolates of Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                               ó
                                                                       01-NOV-1996 (TrEMBLrel. 01, Last sequence update).
01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
STRAIN INDJ-2 RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID-5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (TrEMBLrel. 01, Created)
(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 08, Last annotation update)
RHOPTRY-ASSOCIATED PROTEIN 1 (RAP-1) (FRAGMENT).
                                                                                                                      Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
                                                                                                                                                                                                                                                                                                                                                                                                                         Length 161;
                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Best Local Similarity 100.0%; Pred. No. 4.4e-06;
Matches 17; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                            STRAIN-INDJ-2 (CLONE 2 OF INDIAN ISOLATE J);
MEDLINE-96379224; Pubmed-8784775;
                                                                                                                                                                                STRAIN-INDJ-2 (CLONE 2 OF INDIAN ISOLATE J);
MEDLINE-92244303; PubMed=1574089;
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                                     161 AA
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Mol. Biochem. Parasitol. 51:327-330(1992).
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Mol. Biochem. Parasitol. 77:95-98(1996).
EMBL; U41076; AAC47092.1; -.
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NON_TER 161 161
SEQUENCE 161 AA; 19271 MW; 2433BF4A;
                                                             Created)
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STRAIN-INDC (INDIAN ISOLATE C);
MEDLINE-92244303; PubMed-1574089;
                                                           01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1996 (TrEMBLrel. 01, 01-NOV-1998 (TrEMBLrel. 08,
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SEQUENCE FROM N.A.
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STRAIN INDC R
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Q25764;
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Q27330;
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"Characterisation a sequence of a protective rhoptry antigen from Plasmodium falciparum."
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NCBL_TaxID-5833;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5837;
                                                                 Length 163;
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90023 MW; F69E26A2A564C8EA CRC64;
BD43E37992DF3730 CRC64;
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14, Last annotation update)
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Last annotation update)
                                                               100.0%; Score 84; DB 5; 100.0%; Pred. No. 4.4e-06; ive 0; Mismatches 0;
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STRAIN-HONDURAS I CDC;
MEDLINE-90348711; Pubmed-2200961;
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STRAIN-HONDURAS I CDC;
MEDLINE-92244303; PubMed=1574089;
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19522 MW;
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STRAIN-FUP;
STAIN A:
STRAIN-FUP;
Saul A:
Reficacy of vaccines containing Rhoptry-Associated Proteins RAP1 and
RAP2 of Plasmodium falciparum in Saimiri boliviensis monkeys.";
Submitted (NOV-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AF205283; AAF23404.1;
NON TER 782 782
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                                                                                                                                                                                                                                                            Plasmodium falciparum.
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=5833;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY -ASSOCIATED PROTEIN 1.
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Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 17; Conservative 0; Mismatches 0;
 100.0%; Score 84; DB 5; 1
100.0%; Pred. No. 2.2e-05;
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100.0%; Pred. No. 2.2e-05;
tive 0; Mismatches 0;
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736 LATRLMKKFKAEIRDFF 752
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Best Local Similarity 100.
Matches 17; Conservative
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NCBI_TaxID=5833;
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    Query Match
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Q9U429;
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MEDLINE-90348711; PubMed-2200961;
Ridley R.G., Takacs B., Lahm H.W., Delves C.J., Goman M., Certa V.,
Matlle H., Woollett G.R., Scaffe J.G.;
"Characterisation and sequence of a protective rhoptry antigen from
Plasmodium falciparum.";
MMO1. Blochem. Parasitol. 41:125-134(1990).
EMBL: M32853; AAA29753.1;
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01-UNY-2000 (TrEMBLrel. 14, Last annotation update)
RHOPTRY ASSOCIATED PROTEIN 1 (ROP1) PRECURSOR (FRAGMENT).
Plasmodium falciparum.
Eukaryota, Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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NCBL_TaxID=5833;
                                                                           Length 782;
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                              D1AD099862528D42 CRC64;
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01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPTRY-ASSOCIATED PROTEIN 1 (FRAGMENT).
                                                                         Query Match 100.0%; Score 84; DB 5; I
Best Local Similarity 100.0%; Pred. No. 2.2e-05;
Matches 17; Conservative 0; Mismatches 0;
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Mol. Biochem. Parasitol. 51:327-330(1992).
EMBL; M80807; AAA29717.1; -.
SEQUENCE 782 AA; 90096 MW; DIAD0998625
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01-00V-1996 (TrEMBLrel. 01, Created)
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01-JUN-2000 (TrEMBLrel. 14, Last and
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STRAIN=COLUMBIA;
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01-0CT-2000 (TrEMBLrel. 15, Last annotation update)
01-0CT-2000 (TREMBLrel. 15, Last annotation update)
01-0CT-2000 (TREMBLrel. 15, Last annotation update)
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Fulkaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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NCBL_TaxID=5854;
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NCBL_faxID=5833;
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pred. No. 6.6e-05;
1; Mismatches 0; Indels
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Submitted (FEB-1995) to the EMBL/GenBank/DDBJ databases.
EMBL; U20906; AAA63682.1; -.
SEQUENCE 782 AA; 90160 MW; DE6DIBE2FAC308A9 CRC64;
                                                                                                                                                                STRAIN-FCC1/HN;
Li X.R., Luo S.H., Yu X.B., Shan Z.X., Ma C.L.;
Submitted (NOV-1999) to the EMBL/GenBank/DDJ databases.
EMBL, AF206631; AAFLSS55.1; --
SEQUENCE 782 AA; 90082 MW; 8E1F4CF2883903FD CRC64;
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                                                    Ol-MAY-2000 (TrEMBLrel. 13, Created)
Ol-MAY-2000 (TrEMBLrel. 13, Last sequence update)
Ol-MAY-2000 (TrEMBLrel. 13, Last annotation update)
RHOPPRY ASSOCIATED PROTEIN-1.
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100.0%; Pred. No. 2.2e-05;
iive 0; Mismatches 0;
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SECUENCE OF 216-353 FROM N.A.
Rose M., Hempel S., Entian K.-D., Mewes H.W., Lemcke K., Mayer K.F.X.;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Bukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                     "Structural analysis of Arabidopsis thaliana chromosome 3. I. Sequel features of the regions of 4,504,864 bp covered by sixty Pl and TAC
     s.
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Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Tabata Submitted (JAN-1999) to the EMBL/GenBank/DDBJ databases.
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EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases
EMBL; AL035396; CAA23072.1;
EMBL; AL15539; CAA23072.1;
EMBL; AL15533; CAB81342.1;
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Submitted (FEB-1999) to the EMBL/GenBank/DDBJ databases
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ENVELOPE Protein.
SEQUENCE 1089 AA; 119917 MW; 2ED2EAE60E409C7E CRC64;
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01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                              52.4%; Score 44; DB 10; 66.7%; Pred. No. 91;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         353 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR002419; Feasc_oxidored. Interpro; IPR002493; IPN_synth. Pfam; PF00671; Fe_Asc_oxidored; 1. PRINTS; PR00682; IPNSYNTHASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
                                                                                                                                   MEDLINE=20277480; PubMed=10819329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39933 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
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4. 7:131-135(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SRG1-LIKE PROTEIN.
F24A6.150 OR AT4G25310.
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784 KLLKKFAAEIKD 795
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 RLMKKFKAEIRD 15
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                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SECUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                 [2]
SEQUENCE FROM N.A.
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649 AA; 73892 MW; 3CF9F52B7E5D7505 CRC64;
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                                               Query Match 51.2
Best Local Similarity 81.8
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=3702;
     SEQUENCE
                                                                                                                                                                                                                                               O9XEC5;
                                                                                                                                                                                                                                 Q9XEC5
                                                                                                                                                                                                 RESULT 15
Q9XEC5
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Amanatiaes P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
R.A. Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
R.A. Adams M.D., Celniker S.E., Richards S., Ashburner M., Henderson S.N.,
Sutton G.G., Wortman J.R., Trandell M.D., Zhang O., Chen L.X.,
R.A. Brandon R.C., Rogest Y.-H.C., Blazej R.G., Changhe M., Pfelifer B.D.,
R.A. Annil J.F., Apbayani A., An H.-J., Andrews.Pfannach. C., Baldwin D.,
Ballew R.M., Basu A., Barendale J., Bayraktaroglu L., Basaley E.M.,
Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
Burtis R.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,
R.A. Burtis R.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,
R.A. Burtis R.C., Busam D.A., Buller H., Caddeu E., Center A., Chandra I.,
R.A. Duchin B.D. Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
A Duchon S., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
B. Duchon R.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Duchon K.J., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
A Duchon K.J., Bangelista C.C., Ferraz C., Ferraz C., Ferraz C.,
A Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A.,
A Harris N.L., Harvey D., Heiman T.J., Weil M.-H., Inbeywam C.,
A Barzolo M. Barzolo M. Moy M., Murphy B., Morlecon D.,
A Merkulov G., Milshina N.V., Mobarry C., Morris S., Woller E., Shen H.,
Shue B.C., Siden-Klamos I., Simpson M., Strong R., Pacleb J.M.,
R. She B.C., Standing A.C., Stapleton M., Strong R., Pacleb J.,
R. Williams S.M., Woodage T., Shon M., Zhong G., Zhao O., Zhao O., Zhao G., Zhao G.
                  ö
                                                                                                                                                                                                                                                                  Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                    Gaps
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                    Indels
                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                  1;
   ed. No. 42;
Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FlyBase; FBgn0038435; CG14885.
InterPro: IPR001054; Guanylt_cyclase.
Pfam: PF00211; guanylate_cyc; 1.
PRARY; SM00044; CYCC; 1.
                                                                                                                                                                                            01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last seq
01-JUN-2001 (TrEMBLrel. 17, Last anno
     Pred.
                                                                                                                                                                 PRT;
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 58.3%;
                  7; Conservative
                                                                                                                                                               PRELIMINARY;
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92 LDKFKSDIQDFF 103
                                               6 MKKFKAEIRDFF 17
Best Local Similarity
Matches 7; Conserv
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                                                                                                                                                                                                                                               CG14885 PROTEIN.
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                                                                                                                                                                                                                                                                CG14885
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Q9VEU6
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                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
Surosids II; Brassicales; Brassicacee; Arabidopsis.
                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
Zhong J., Ma P., Parnell L.D., Chen C.-N., Chen E.Y.;
"Genomic sequence of Arabidopsis thaliana BAC T26N6, chromosome IV, 19 3 cm."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. Zhong J. Ma P., Parnell L.D., Chen C.N., Chen E.Y.; Mewes H.W., Lemcke K., Mayer K.E.X.; Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
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Length 649;
                                            Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AF076243; AAD229760.1; -.
EMBL; ALI01500; CAB77916.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (MAY-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hypothetical protein.
SEQUENCE 398 AA; 43961 MW; 0077BE2298E94AD7 CRC64;
                                                                                                                                                                                                                                                                         01-NOV-1999 (TrEMBLrel. 12, Created)
01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
01-NOY-1999 (TrEMBLrel. 15, Last annotation update)
HYPOTHETICAL 44.0 KDA PROTEIN.
T26N6.8 OR AT4G04480.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2
  5;
Score 43; DB 5
Pred. No. 78;
1; Mismatches
                                                                                                                                                                                                                                        398 AA.
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Pred. No. 70;
1; Mismatches
                                                                                                                                                                                                                                        PRT;
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60.0%;
  51.2%;
81.8%;
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Best Local Similarity 60.0.
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546 LALRVMKKFKA 556
                                                                                 1 LATRIMKKFKA 11
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Pathogen derived T T helper cell (Th) Unidentified pepti Amino acid residue Amino acid sequenc

Antigenic fragment Antigenic fragment Peptide 5 for pept HIV-derived lipope HLA class II bindi

Human APP A-beta 1 PSMpep007 - P2 ins PSMpep008 - P2 ins PSMpep009 - P2 ins

Tetanus toxoid 830 Tetanus toxoid 830 Tetanus toxoid epi

Tetanus toxin T-ce HER-2 B cell pepti Tetanus toxoid TTB Tetanus toxoid TT T-cell stimulatory Clostridium tetani

Helper T cell epit Tetanus toxin help Tetanus toxin help T-cell antigen TT2 HLA class II bindi

Perfect score:

Run on:

Sedneuce:

Scoring table:

Searched:

Database :

Tetanus toxoid pro Wild-type TT830 (t

Amino acid sequenc Clostridium tetani Tetanus Toxoid uni

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Synthetic peptide(s) corresp. to tetanus toxin epitope(s) - used as universal carriers for prepn. of immunogenic conjugate(s) for
                                                                                                                                                                                                                                                                                      Tetanus toxin; vaccine; major histocompatibility complex; MHC; antimalarial.
                                                                                                                                                                                                                                                                                                                                                                                    Corradin G;
                                                                                                                                                                                                              ALIGNMENTS
                                                                                                                                                                            AAB46203
AAY92650
AAY92651
AAY92652
                                                   AAW35445
AAY29705
AAR82573
AAR82573
AAW0559
AAY89274
AAY56056
AAY560904
AAY58768
                                                                                                                                  AAB31118
AAB15589
AAY26607
AAY99055
                                                                                                                                                          AAB46175
AAB46178
           AAY44763
                       AAB61956
                             AAB20143
                                  AAB68636
                                        AAB46172
                                              AAB49071
                                                                                                                                                                      AAB46196
                 AAB85451
                                                                                                                                                                                                                                                                                                                                                                                    Verdini AS,
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                                                                                                                                                                                                                                           AAR06310 standard; protein; 15
                                                                                                                                                                                                                                                                                                                                                       89IT-0022409.
                                                                                                                                                                                                                                                                                                                                            89EP-0203318
                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                                                                                                                                                                        (ENIE ) ENIRICERCHE SPA.
 Tetanus toxin epitope
                                                                                                                                                                                                                                                                                                                                                                                    Pessi A, Bianchi E,
                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1990-225582/30.
use as vaccines.
                                                                                                                                                                                                                                                                                                                                           27-DEC-1989;
                                                                                                                                                                                                                                                                                                                                                       16-NOV-1989;
17-JAN-1989;
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                                                                                                                                                                                                                                                                                                                                25-JUL-1990
                                                                                                                                                                                                                                                                                                                    EP378881-A.
                                                                                                                                                                                                                                                                                                          Synthetic.
AAR06310;
                                                                                                                                                                                                                                    AAR06310
RESULT
                                                                                                                                                                                                                                                       Universal helper T
T-Helper epitope f
T-cell epitope pep
Tetanus toxoid epi
Tetanus toxoid epi
Tetanus toxoid T C
Foreign epitope P2
                                                                                                                                                                                                                                                                                                                                                                    Tetanus toxin epit
                                                                                                                                                                                                                                                                                                                                                                        Universal T-cell e
Tetanus toxoid uni
                                                                                                                                                                                                                                                                                                                                                                                   Tetanus toxin frag
                                       Search time 66.28 Seconds (without alignments)
16.764 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                        GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                      522463 segs, 74073290 residues
                                        ٠.
                                                                                                                                                                                                                                                                                                                                      SUMMARIES
                                       January 29, 2002, 10:59:19
                                                                                                                                              Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                  AAR06310
AAW35506
                                                                                                                                                                                                                                                                                                                                                                                        AAW71321
AAY04051
AAW67578
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AAY82637
AAY92625
                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                              AAW11505
                                                                                                                                                                                                                                                                                                                                                                                                           AAW73220
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                                                                                     BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                         1 QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                       ΩI
                                                               US-09-763-397A-24
                                                                                                                            Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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100.0
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Score

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QYIKANSKFIGITEL 15
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                                                                                                                                                                        Best Local Similarity
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                                                                                            AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein;
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                                                                                                                                                                                          Matches
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                                                                                                                                                                                                                                                                    qq
through a linker to a solid phase, forming a complex of (A)-solid phase.

through a linker to a solid phase, forming a complex of (A)-solid phase.

where (A) comprises 10-50 annho acids capable of forming a secondary

structure in a benign buffer after liberation from the solid phase, and

further the (A)-solid phase complex comprises an immunogenic substance

and/or an immune mediator coupled on (A). The present sequence

represents a peptide used in an example from the present invention. An

(A)-solid phase complex can be used as a scaffold for the production of

chemical derivatives, characterised by covalently attaching molecules at

attachment points. Alternatively (A) is used as a scaffold-peptide for

the incorporation into an Immunostimulating Complex (Iscom) resulting an

(A)-iscom complex which is used for the chemical coupling of antigenic

substances in an aqueous solution by conjugation. (A) derivatised with

one or more peptides having fibronectin-, laminin- or vitronectin-like

binding activities can be used for the promotion of cell-attachment to

plastic surfaces, in particular to inhibit tumour growth and metastasis,

and for promotion of wound healing. Also a derivatised (A) can be used
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               T-cell stimulatory peptide; immunogen; non-dendritic; carrier; tumour; scaffold; inhibition; metastasis; wound healing; solid phase.
                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Non-dendritic peptide carrier linked to a solid phase - useful as diagnostic agent and as a scaffold for production of chemical
                                  Epitopic peptides may be used with synthetic hapten derived from a pathogen to generate an immune response to the pathogen. Peptides are recognised by numerous T-helper cell clones within the context of a wide range of alleles of the human MHC. The peptides may be used in an antimalarial vaccine inducing Ab.
                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                              100.0%; Score 74; DB 11; Length 15; 100.0%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                      ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Universal T-cell epitope peptide SEQ ID NO:8.
                                                                                                                                                                                                                                                                      Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                               AAW35506 standard; peptide; 15 AA.
Claim 1; Page 17; 20pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       22-APR-1998 (first entry)
                                                                                                                                  response to P.falciparium.
                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                1 QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PEPR-) PEPRESEARCH AS.
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Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                      15 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unidentified
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for the selection of specifically-binding aptamers or as a diagnostic agent. Such diagnostic.(A) molecules could be used to detect molecules derived from or indicative of pregnancy or of a disease, such as an infectious, autoimmune or cancerous disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                                                                                                                                                      Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Humanised antibody; anti-Fc receptor; H22; bifunctional; bispecific; fusion protein; chimera; tetanus toxoid; helper T cell epitope;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Recombinant, multi-specific anti-Fc receptor antibody molecules also comprise an anti-target portion, used for the treatment of cancer, autoimmune disease and pathogenic infection
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100.0%; Pred. No. 2.3e-07;
tive 0; Mismatches 0;
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                                                                                                                                                                                                                                        100.0%; Score 74; DB 18; 100.0%; Pred. No. 2.3e-07;
                                                                                                                                                                                                                                                                                                   0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tetanus toxoid universal Th epitope TT830.
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                                                                                                                                                                                                                                                                                                      15; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                1 gyikanskfigitel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (MEDA-) MEDAREX INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1997-052242/05
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Best Local Similarity
Matches 15; Conserv
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AAW67033

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AAW71321-22 represent universal helper T-cell epitopes derived from tetanus toxin. They are used to enhance host immune response to vaccines. The specification describes a Plasmodium yoelil liver stage 17 kDa hepatic and erythrocytic stage protein designated PyHEDI7. This protein elicits a response from an Igl monoclonal antibody designated Navy Yoelii Liver Stage 3 (NVLS3). This antibody does not recognise sporozoites, but does recognise P. Yoelii liver stage parasites. NVLS3 eliminates upto 90% of liver stage parasites. The specification by a malaria parasite of the genus Plasmodium. The DNA vaccine comprises evon 1 and part of exon 2 of the PyHEPI7 gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmodium species - comprises a first nucleic acid encoding a first polypeptide capable of eliciting an immune reaction against an antigen expressed during the liver
                                                                                                                                                    Liver stage, Plasmodium, Navy Yoelli Liver Stage 3 antibody; NYLS3; hepatic and erythrocytic stage protein; PyHEP17; vaccine; malaria parasite; teanus toxin; P2; helper T-cell epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Covalently reactive antigen analog; CRAA; catalytic antibody; electrophilic reaction centre; phosphonate; boronate; vaccine; transition state analog; TSA; isostere; gpl20; HIV-1; T-helper; tetanus; toxoid; B-T-epitope.
                                                                                                              Universal helper T-cell epitope P2 derived from tetanus toxin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Hedstrom RC, Hoffman SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 100.0%; Score 74; DB 19; 100.0%; Pred. No. 2.3e-07;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-Helper epitope from tetanus toxoid
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                                                                                                                                                                                                                                                                                                                                                                                                94US-0319704.
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                                                                   26-NOV-1998 (first entry)
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es 15; Conservative
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                                                                                                                                                                                                                                                                  Clostridium tetani.
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                                                                                                                                                                                                                                                                                                                                                                                                07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                         07-0CT-1994;
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                                                                                                                                                                                                                                                Synthetic.
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                          AAW71321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to a new carbohydrate peptide conjugate, which comprises a carrier with a dendrimeric poly-lysine enabling multiple epitopes to be covalently attached to it. Also claimed are: (1) an antibody purified from biological fluid or cells of organisms administered with the carbohydrate peptide conjugate, and (2) a diagnosis of tromprising antigen-specific antibodies elicited by immunisation with the carbohydrate peptide conjugate. The peptide conjugate, antibody and carbohydrate peptide conjugate. The peptide conjugate, antibody and diagnosis kit are used to provide pharmaceutical compositions and carbohydrate peptide conjugate and response against tunours. These can be used to support an immune response against viral infections caused by hepatitis virus, HIV or cytomegalo virus. They can be used to enhance immune responses, especially 8- and 7-cell responses, of humans and animals against bacterial infections. The carbohydrate peptide conjugate stimulates the antibody and T-cell response without stimulating undeslired immune responses. The composition animals. The present sequence corresponds to residues 830-844 of tetanus toxin. The synthetic peptide corresponding to this sequence may be used an epitope in a carbohydrate peptide conjugate.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Carbohydrate peptide conjugate used as vaccine - comprises carrier with dendrimeric poly-lysine enabling multiple epitopes to be covalently attached
                                                                                                                                                                                                                                                                                                        Tetanus toxin: vaccine; antibody; carbohydrate peptide conjugate; dendrimeric poly-lysine; epitope; tumour.
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100.0%; Pred. No. 2.3e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lo-man R;
                                                                                                                                                                                                                                                                Tetanus toxin fragment (residues 830-844).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 13; 55pp; English.
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                                                                                                                                AAW67033 standard; peptide; 15 AA.
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Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                          AAW67033;
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AAW71321

Length 15; Indels

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The patent discloses new covalently reactive antigen analogs (CRAA)

of formula X1-Y-E-X2, in which X1 and X2 represent peptide sequences

of an epitope of a disease-associated protein, Y is a positively

charged amino acid residue, preferably Lys or Arg, and E is an

electrophilic reaction centre, preferably by or Arg, and E is an

electrophilic reaction centre, preferably a phosphonate or boronate

coniety. Depending on the identity of the epitope, the CRAA may be used

to stimulate production of catalytic antibodies specific for

predetermined antipodies associated with particular medical disorders.

They may also be used to permanently inactivate endogenously produced

catalytic antibodies produced in certain autoimmune diseases as well as

in certain lymphoproliferative disorders.

Amongst the specifically exemplified CRAAs is one based on residues

to counter HIV-1 infections. When used as an immunogen, preferably this

to counter HIV-1 infections. When used as an immunogen, preferably this

catalytic antipodated at its N-terminal to a T-heiper epitope from tetanus

covincer HOV present sequence represents the T-heiper epitope and

covince TAPA present sequence represents the T-heiper epitope and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chimeric; non-typable Haemophilus influenzae; fimbrin; T-cell epitope; immunogenic composition; immune response.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    T-cell epitope peptide #4 for chimeric fimbrin/T-cell epitope peptide.
                                                                                                                                                                                                                                                                                New covalently reactive antigen analogs used for treating e.g. autoimmune diseases, lymphoproliferative disorders, cancers, microbial infections, ischemic and reperfusion injury or septic shock \cdot
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100.0%; Pred. No. 2.3e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                      Disclosure; Page 86; 158pp; English.
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                                                                                                                                                                                                                     Smith
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                                                                                                                                                                                                                     Gololobov G,
                                                                                                                                                                                                                                                     WPI; 1999-591076/50.
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Best Local Similarity
                Clostridium tetani.
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                                                                                                                  23-MAR-1999;
                                                                                                                                                    23-MAR-1998;
                                                  W09948925-A1
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The invention relates to the manufacture of a synthetic chimeric peptide comprising a non-typable Haemophilus influenzae fimbrin peptide fused vla a linker peptide to a T-cell epitope peptide. The chimeric peptide is used in immunogenic compositions which induce an immune response against non-typable Haemophilus influenzae. This sequence represents an example of a T-cell epitope peptide used to generate the chimeric peptide.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multispecific single chain antibody; antibody H22; tumour cell; therapy; antibody-dependent cellular cytotoxicity; ADCC; HER 2/neu; infection; epidermal growth factor receptor; breast cancer; ovarian cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Specific killing of tumour cells - using a multi-specific molecule comprising an anti-Fc receptor antibody and a portion which binds to a target cell
                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This sequence represents a tetanus toxoid epitope and is recognised by the multispecific single chain antibody designated H22. The antibody can be used in the method of the invention for inducing
                                                                                                            Synthetic chimeric fimbrin peptide - useful for vaccination against non-typable Haemophilus influenzae
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                                                                                                                                                                                                                                                                                                                    100.0%; Score 74; DB 20;
100.0%; Pred. No. 2.3e-07;
:ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 7; Column 27; 57pp; English.
                                                                                                                                                          Disclosure; Column 4; 16pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAW73220 standard; Protein; 15 AA.
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        95us-0460502.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                              Kaumaya PTP;
                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.
nes 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                            1 QYIKANSKFIGITEL 15
                                  (OHIS ) UNIV OHIO STATE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Tetanus toxoid epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Goldstein J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-023374/02.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (MEDA-) MEDAREX INC.
                                                                                        WPI; 1999-044514/04
                                                                                                                                                                                                                                                                                    15 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           07-JUN-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     07-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-JAN-1999
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        US5837243-A.
        02-JUN-1995;
                                                               Bakaletz LO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-NOV-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Synthetic.
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Best Local Si
Matches 15,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAW73220;
                                                                                                                                                                                                                                                                                      Sequence
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Gaps

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Indels

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Mismatches Pred. No.

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Best Local Similarity 100.
Matches 15; Conservative
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antibody-dependent cellular cytotoxicity (ADCC) against a tumour cell which is characterised by overexpression of HER 2/neu or epidermal growth factor receptor (EGER), comprises contacting the tumour cell with a multispecific protein molecule (preferably a single chain antibody) comprising: (a) an anti-Fc receptor antibody or an antigen binding fragment; (b) a portion which binds to HER 2/neu; and (c) a portion which binds to EGFR. The method can be used for treating cancers especially breast cancer or ovarian cancer. The multispecific antibody can also be administered prophylactically to vaccinate a subject against infection
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention is concerned with methods of treating asthma, eosinophilia, allergic rhinitis and other allergic diseases. These involve the use of interleukin-5 (IL-5) analogues and modified IL-5 proteins and their coding sequences to down-regulate IL-5 activity and thus reduce eosinophil numbers. The allergic diseases may be treated using autovaccines, nucleic acid vaccines or live vaccines. In addition, it is possible that they may be used in the treatment of cancer and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Asthma; IL-5; interleukin-5; allergy; cytokine; helminthic infection; cancer; eosinophilia; vaccine; allergic rhinitis.
                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Down-regulating interleukin 5 (IL-5) activity in humans by administering IL-5 and/or an IL-5 analogue, useful in the treatment, prophylaxis or amelioration of asthma or other chronic allergic conditions -
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                                                                                                                                                                                                                                   Length 15;
                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                   100.0%; Score 74; DB 20; 100.0%; Pred. No. 2.3e-07;
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                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                    AAB45511 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetanus P2 epitope SEQ ID NO: 23.
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99US-0132811.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   26-FEB-2001 (first entry)
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                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                 1 QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                      nelminthic infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2000-672791/65.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clostridium tetani.
                                                                                                                                                                                                                                               Best Local Similarity
Matches 15; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15 AA;
                                                                                                                                                                                     15 AA;
                                                                                                                                                     by a target cell.
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06-MAY-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Klysner S;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAB45511;
                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                   Query Match
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The present invention describes a compound (I) for the prevention and/or treatment of allergy. The compound comprises at least one allergen antigenic determinant (i) recognised by a B cell or an antibody secreted by a B cell of a non-atopic individual and at least one antigenic determinant (ii) different from the allergen that triggers T cell activation. (I) has antiallergic, antiasthmatic. antinflammatory. defemmatological and immunosuppressive activities, and can be used in a vaccine. (I) may be used in a planaecettical or cosmetic medicament to treat and/or prevent allergies or a disease of allergic origin, especially hypersensitivities. These include rhintis, slustis,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bronchial asthma, atopic dermatitis, some forms of acute and chronic urticaria, gastro-intestinal syndromes associated with the ingestion of food allergens, oro-pharyngeal syndrome, anaphylactic reactions associated with drug hypersensitivities and/or a mixture of these. The use of (I) in the treatment of allergic conditions avoids the need for drug treatment, which often causes undesirable side-effects. Also, prior art drug therapies alleryiate symptoms, but do not influence their causes, however (I) actually combats the cause of an allergic reaction. The present sequence represents a peptide, which is used in an example from the present invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antiallergic; antiasthmatic; antiinflammatory; dermatological; immunosuppressive; vaccine; rhinitis; sinusitis; bronchial asthma; atopic dermatitis; acute urticaria; chronic urticaria; gastro-intestinal syndrome; food allergen; oro-pharyngeal syndrome; anaphylactic reaction; drug hypersensitivity; allergic reaction.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     epitope; B cell epitope; allergy; allergen; antigenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Tetanus toxoid T cell epitope peptide SEQ ID NO:13.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Example 6; Page 30; 50pp; English.
                                                                                                                                                                                                                                                                                       AAY82637 standard; peptide; 15 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Jacquemin M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
        15
                                              1 QYIKANSKFIGITEL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20-JUL-1999;
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AA;

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Sequence

100.0%; Score 74; DB 21; Length 15;

Query Match

us-09-763-397a-24.rag

Osteoprotegerin ligand, OPGL, osteoprotegerin, osteoclastogenesis; tumour necrosis factor receptor; type II transmembrane protein; osteoclast differentiation; CSF-1; osteoclast activator; immune response; osteoporosis; bone resorption;

tetanus toxoid P2 epitope.

Clostridium tetani.

WO200015807-A1.

23-MAR-2000

Amino acid sequence of the tetanus toxoid P2 epitope.

25-JUL-2000 (first entry)

AAY84427;

AAY84427 standard; Peptide; 15 AA.

RESULT 12

AAX84427

1 qyikanskfigitel 15

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The claims detail a method for inducing immune responses against weakly immunogenic cell-associated peptide antigens (PA) such as those associated with cancers (i.e. self-proteins), for example, human prostate specific membrane antigen (PSM), hersqulin 2 (Her2) and/or fibroblast growth factor 8b (FGF8b). The method comprises effecting simultaneous presentation by antigen producing cells (APCS) of the animals immune system of: (1) at least 1 CTL (cytotoxic T-lymphocyte) group derived from the PA and/or at least 1 B-cell group derived from the foreign to the animal. Analogues of human PSM, human Her2 and human/murine FGF8b comprising a substantial part of all known and predicted CTL and B-cell epitopes of the respective PA and including at least one foreign T helper epitope (e.g. P2 and/or PN) are also claimed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The method is used to treat prostate, prostate/breast or breast cancer when the PA is human PSM, FGF8b and Her2, respectively.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Dalum I;
                                                                                                                                                                                                                                                                                                  Foreign epitope, P2; prostate specific membrane antigen; PSM; Her2; Heregulin 2; Fibroblast growth factor 8b; FGF8b; vaccination; cytotoxic T-lymphocyte immunity; self-protein; cancer; breast cancer; prostate cancer; cell-associated peptide antigen.
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nielsen KG, Haaning J, Leach D,
100.0%; Score 74; DB 21; Length 15; 100.0%; Pred. No. 2.3e-07; .ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 1; Page 213; 220pp; English.
                                                                                                                                                                            AAY92625 standard; Protein; 15 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Karlsson G;
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98US-0105011.
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                                  Conservative
                                                                1 OYIKANSKFIGITEL 15
                                                                                 Birk P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2000-349917/30
                                                                                                                                                                                                                                                                                                                                                                                      Clostridium tetani.
                                                                                                                                                                                                                                                                        Foreign epitope P2.
   Query Match
Best Local Similarity
Matches 15; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Steinaa L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gautam A,
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98DK-0001164. 99WO-DK00481

15-SEP-1998; 02-OCT-1998; 13-SEP-1999;

(MEBI-) M & E BIOTECH AS.

Haaning J;

Halkier T,

WPI; 2000-271444/23

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              used to create a fusion protein with murine osteoprotegerin ligand (OPGL). Osteoprotegerin is a secreted member of the tumour necrosis dependent manner. The OPGL protein is synthesised as a type II transmembrane protein. The murine and human OPGL polypeptides are B7% transmembrane protein. The murine and human OPGL polypeptides are B7% transmembrane protein. The murine and human OPGL polypeptides are B7% transmembrane protein. The murine and human OPGL polypeptides are B7% differentiation in the absence of CSF-1. OPGL is also an activator of differentiation in the absence of CSF-1. OPGL is also an activator of down-regulation of OPGL activity in an animal. The method comprises using at least one OPGL polypeptide or subsequence, and/or at least one oPGL polypeptide are useful for treating, preventing and ameliorating osteoporosis or other diseases or conditions characterised by excessive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                In vivo down-regulation of osteoprotegerin ligand (OPGL) activity used to treat, prevent and ameliorate osteoporosis -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   present sequence represents the tetanus toxoid P2 epitope. It
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100.0%; Pred. No. 2.3e-07;
iive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          bone resorption.
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Gaps

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Indels

100.0%; Score 74; DB 21; 100.0%; Pred. No. 2.3e-07; iive 0; Mismatches 0;

Local Similarity 100. nes 15; Conservative

Best Loca Matches

Query Match

1 QYIKANSKFIGITEL 15

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Length 15;

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Tetanus toxoid protein derived T-cell activating epitope P2.
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                                                                                                                                                                                                                               Clostridium tetani.
                                                                                                                                                                                                                                                                                             WO200004170-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                             L4-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              14-JUL-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Smit J;
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NOT COULD COURSE AND ANALYSE A
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                                                                                                                                                                                                                     Recombinant protein; CDC/NIIMALVAC-1; multivalent; malaria; vaccine; T-cell epitope; treatment; tetanus toxoid; antigenic epitope; treatment; cricumaporozoite protein; CSP: sporozoite surface protein-2; SSP-2; liver stage antigen-1; LSA-1; merozoite surface protein-1; MSP-1; MSP-2; apical membrane antigen-1; AMA-1; erythrocyte binding antigen-175; EBA-175; rhoptry associated practin-1; RAP-1; gamete specific antigen; Pfg27; antiparasitic; prevention; anti-CDC/NIIMALVAC-1 antibody.
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                                                                                                                                                          Clostridium tetani tetanus toxoid T-cell epitope, P589.
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100.0%; Pred. No. 2.3e-07;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ¥.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (NAIM-) NAT INST IMMUNOLOGY.
                                                                                         06-JUN-2000 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Clostridium tetani.
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Matches 15; Conserv
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                           AAY70300;
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which is produced by Caulobacter and consists of Caulobacter surface layer (S-layer) protein (containing the C-terminal secretion signal) and a target protein heterologous to Caulobacter. The cleavage of target protein from the S-layer protein is carried out under mild acid conditions so that cleavage occurs at aspartate-proline dipeptide site without solubilising the protein. The cleavage is accomplished while the fusion protein is in an insoluble agraced form which facilitates purification of the protein. The method is useful for producing pure proteins including recombinant human and animal therapeutic antibiotic and vaccine peptides, enzymes, protein polymers, and antibacterial enzymes for foodstuffs.

The present sequence is a T-cell activating epitope P2 derived from tetanus toxold protein. This sequence was fused to a DNA encoding a fragment of Infectious pancreatic necrosis virus surface glycoprotein which is a vaccine candidate. This chimeric protein was in turn fused to DNA encoding C crescentus S-layer secretion signal (corresponds to the C-terminal portion of the S-layer protein from amino acid 690 onwards and contains native Asp Pro site) for construction of a recombinant contains native Asp Pro site) for construction of then cleaved
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
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Surface layer protein; S-layer secretion signal; antibiotic; vaccine; recombinant fusion protein cleavage; enzyme; protein polymer; foodstuff; antibacterial enzyme; surface glycoprotein; T-cell activating epitope; P2; tetanus toxoid; IPNV; Infectious pancreatic necrosis virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 produced recombinant fusion proteins useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               patent discloses a method for cleaving a recombinant fusion protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to recover the vaccine candidate protein.
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The invention relates to a new method for inducing killing of a tumor cell which expresses HER 2/neu or epidermal growth factor receptor feGFR). The method comprises contacting the tumor cell with a multispecific protein comprising a component, preferably an antibody, which binds to an Fc receptor (FcR), Her 2/neu or EGFR. The method is useful for inducing killing of a tumor cell from breast cancer, sarcoma, carcinoma, or ovarian cancer. Specific multispecific proteins can also be administered to a subject to treat or prevent other diseases or conditions, including pathogenic infections (e.g., viral (such as HIV)), protozoan infections (such as Toxoplasma gondii), fungal infections (such as candidiasis), and an autoimmunity (e.g. immune thrombocytopenia purpura and systemic lupus). The present sequence represents a wild-type tetanus toxin TT830 epitope.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Inducing killing of tumor cells which expresses HER 2/neu or epidermal growth factor receptor (EGFR) by contacting the cell with multispecific proteins comprising an anti-Fc receptor, -Her 2/neu or -EGFR antibody, useful for treating cancer -
Fc receptor; FcR; tumor cell; breast; cancer; sarcoma; carcinoma; HIV; pathogenic; Toxoplasma gondii; candidisats; systemic lupus; cytostatic; immune thrombocytopenia purpura; immunosuppressive; antiviral; antifungal; antiprotozoal; TT830; tetanus toxin.
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95US-0484172.
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                                                                                                                                                                                                                    Clostridium tetani
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Query Match Best Local Similarity Matches 15; Conserv Qy

Search completed: January 29, 2002, 10:59:20 Job time: 2244 sec

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APPLICANT: Hoffman, Stephen L.
APPLICANT: Hedstrom, Richard C.
APPLICANT: Hedstrom, Richard C.
APPLICANT: Hedstrom, Richard C.
TITLE OF INVENTION: Protective 17 kbm Malaria Hepatic and TITLE OF INVENTION: Brythrocytic Stage Immunogen and Gene NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Naval Medical R & D Command
STREET: Bldggl, T-12, 8901 Wisconsin Avenue
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Pred. No. 1.2e-07;
PCT-US95-02121-95
PCT-US92-07218-25
PCT-US92-07218-31
PCT-US95-02121-110
PCT-US92-07218-26
PCT-US92-07218-26
PCT-US92-07218-27
PCT-US92-07218-32
PCT-US95-02121-111
PCT-US95-02121-112
US-09-075-257A-13
US-09-075-257A-14
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US-09-171-969-7
US-08-661-052-9
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NAME: A. David Spevack
REGISTRATION NUMBER: 24,743
REFERENCE/DOCKET NUMBER: 75
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24,743
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100.0%;
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INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acids
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Best Local Similarity 100.
Matches 15; Conservative
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    CITY: Bethesda
STATE: Maryland
    TOPOLOGY:
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                                                                                                     Search time 32.24 Seconds (without alignments) 10.470 Million cell updates/sec
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Sequence 55,
Sequence 4, A
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Sequence 13,
Sequence 63,
Sequence 57,
Sequence 57,
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Sequence 6
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Sequence 6
Sequence 3
Sequence 3
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/cgn2_6/ptodata/2/jaa/5B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6A_COMB.pep:*
/cgn2_6/ptodata/2/jaa/6B_COMB.pep:*
/cgn2_6/ptodata/2/jaa/FCTUS_COMB.pep:*
/cgn2_6/ptodata/2/jaa/PCTUS_COMB.pep:*
                4.5
Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                    212252 seqs, 22503292 residues
                                                                                                        ٠.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SUMMARIES
                GenCore version
Copyright (c) 1993 - 2000
                                                                                                     January 29, 2002, 10:59:58
                                                                                                                                                                                                                                                                                                                                                                      Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                          sw model
                                                                                                                                                                                                                       BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                          1 QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  score greater than or equal to
and is derived by analysis of
                                                                          protein search, using
                                                                                                                                                       US-09-763-397A-24
                                                                                                                                                                                                                                                                                                                              seq length: 0 seq length: 2000000000
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Match I
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Score

Result Š g

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GENERAL INFORMATION:
APPLICANT: Sudhir Paul
APPLICANT: Sudhir Paul
APPLICANT: Sudhir Paul
APPLICANT: Gennady Gololobov
TITLE OF INVENTION: Inhibitors of Catalytic Antibodies, Compositions and Their
TITLE OF INVENTION: Use
FILE REFERENCE: UNNC 63123
CURRENT APPLICATION NUMBER: US/09/046,373
CURRENT APPLICATION NUMBER: US/09/046,373
CURRENT FILING DATE: 1998-03-23
NUMBER OF SEQ ID NOS: 10
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 74; DB 2; Length 15; Best Local Similarity 100.0%; Pred. No. 1.2e-07; Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100.0%; Score 74; DB 4; Length 15; 100.0%; Pred. No. 1.2e-07;
                                                                                                                       OFFICIAL STATES SOFTING #1.25 SOFTING #1.25 CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/460,502
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                         22727/00120
                                                               MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                 CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: GOLTICK, Mary E.
REGISTRATION NUMBER: 34,829
REFERENCE/DOCKET NUMBER: 22727
TELECOMMUNICATION INFORMATION:
TELEPHONE: (216) 622-8458
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; Sequence 6, Application US/09188082; Patent No. 6270765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; Sequence 2, Application US/09046373; Patent No. 6235714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQ ID NO 2
LENGTH: 15
TYPE: PRT
CRGANISM: Clostridium tetani
US-09-046-373-2
                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 15 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 QYIKANSKFIGITEL 15
                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-460-502-7
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                                                                                                                                                                                               FILING DATE: CLASSIFICATION:
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  COUNTRY:
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APPLICANT: Kaumaya, Parvin T.
TITLE OF INVENTION: Synthetic Chimeric Fimbrin Peptides
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Calfee, Halter and Griswold
STREET: Gloo Superior Avenue
CITY: Cleveland
STATE: Ohio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                APPLICANT: Yashwant M. Deo
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 74; DB 2;
Pred. No. 1.2e-07;
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                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/484,172
FILING DATE: 07-JUNE-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Arnold, Beth E. REGISTRATION NUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/661,052
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 7, Application US/08460502 Patent No. 5843464
                                                                                                     ; Sequence 6, Application US/08661052
; Patent No. 5837243
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100.0%;
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INFORMATION FOR SEQ ID NO: 6:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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1 QYIKANSKFIGITEL 15
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                                                                                                                                                    GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                               RESULT 2
US-08-661-052-6
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US-08-460-502-7
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Patent No. 6231864
GENERAL INFORMATION
TITLE OF INVENTION: Strategically Modified Hepatitis B Core Proteins and
TITLE OF INVENTION: their Derivatives
FILE REFERENCE: SYN-101 4564/6929
CURRENT APPLICATION NUMBER: 08/09/248,588
CURRENT FILING DATE: 1999-02-11
EARLIER APPLICATION NUMBER: 60/074537
EARLIER FILING DATE: 1998-02-12
NUMBER OF SEQ ID NOS: 113
SOFTWARE: PatentIn Ver. 2.0
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Pred. No. 1.3e-07;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 74; DB 5; 1 100.0%; Pred. No. 1.2e-07;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
TLING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REFERENCE/DOCKET NUMBER: 022.101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 510-601-2706
TELEPHONE: 510-65-35-35
INFORMATION FOR SEQ ID NO: 69:
SEQUENCE CHARACTERISTICS:
LENGTH: 15 amino acids
TYPE: amino acid
STRANBONESES: 11ngle
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Best Local Similarity 100.0%;

Matches 15; Conservative 0
        28-DEC-1993
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ORGANISM: Clostridium tetani
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                                                                                                                                                                                 linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               JOURNAL: Vaccine VOLUME: 15
                                                                                                                                                                                                                                                                                                                                                                                           PCT-US93-11703-69
                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-248-588-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; DATE: 1997
US-09-248-588-55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  US-08-446-692-4
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LENGTH: 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Indels
GENERAL INFORMATION:
APPLICANT: Yashwant M. Deo
APPLICANT: Joel Goldstein
APPLICANT: Joel Goldstein
APPLICANT: Chezian Somasundaram
TITLE OF INVENTION: THERAPEUTIC COMPOUNDS COMPRISED
TITLE OF INVENTION: OF ANTI-FC RECEPTOR ANTIBODIES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: LAHIVE & COCKFIELD
STREET: 60 State Street, Suite 510
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: 1BM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/11703
                                                                                                                                                                                                                                                                              ZIP: 02109-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/188,082
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PCT-US93-11703-69
Sequence 69, Application PC/TUS9311703
GENERAL INFORMATION
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF EXQUENCES: 75
CORRESPONDENCE ADDRESS:
ADDRESSEE: Grant D. Green
STREET: 4560 Horton St.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INPORMATION:
NAME: ATROId, Beth E.
REGISTRATION INUMBER: 35,430
REFERENCE/DOCKET NUMBER: MXI-043CP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
INPORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERIŞTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/661,052
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Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: peptide FRAGMENT TYPE: internal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 OYIKANSKFIGITEL 15
                                                                                                                                                                                                                                               Massachusetts
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                                                                                                                                                                                                                              Boston
                                                                                                                                                                                                                                                                    COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-188-082-6
                                                                                                                                                                                                                                                 STATE:
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Gaps
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Patent No. 6090388

GENERAL INFORMATION: GENERAL INFORMATION: PEPTIDE COMPOSITION FOR TITLE OF INVENTION: PREVENTYON AND TREATMENT OF HIV INFECTION AND TITLE OF INVENTION: IMMUNE DISORDERS

TITLE OF INVENTION: IMMUNE DISORDERS

NUMBER OF SEQUENCES: 66

CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 17;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 74; DB 2; I
100.0%; Pred. No. 1.4e-07;
iive 0; Mismatches 0;
                                                                                CLASSIFICATION: 424
PRIOR APPLICATION 1 424
PRIOR APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION A 424
PRIOR APPLICATION DATE:
APPLICATION NUMBER: US 08/057,166
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MATIA C.H. LIN
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, Version SOFTWARE: #1.25 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/100,409A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER:
REFERENCE/DOCKET NUMBER: 1151-4154
TELECOMMUNICATION:
TELEPHONE: 212-758-4800
TELEPAX: 212-751-6849
                                              US 08/446,692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORGAN & FINNEGAN STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                  REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                  TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 aming acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       : 345 Park Avenue
New York
                                                           7-JUN-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: peptide
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 10154-0054
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FILING DATE:
CLASSIFICATION:
                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US-09-100-409A-40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          US-08-488-351A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              q
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Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ;
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Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 15; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FIJ.NG DATE: 7-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25 CURRENT APPLICATION BATA: APPLICATION NUMBER: US/08/446,692 FILING DATE: 7-JUN-1995 CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY AGENT INFORMATION:
NAME: Maria C.H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
                                                                                                                                                                                                                                                                 ZIP: 10154-0053
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISILES:
LENGTH: 17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEE: Maria C.H. Lin
1: 345 Park Avenue
New York
                                                                                                                                                       ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-446-692-4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 QYIKANSKFIGITEL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
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STATE:
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Sequence 7, Application PC/TUS9513841 GENERAL INFORMATION:
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Best Local Similarity
Matches 15; Conserva
                                                                                                                                                           STREET: 345 Par
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New York
                                                                                                                                                                                                                USA
                                                                                                                                            ADDRESSEE:
                                                                                                                                                                                                                               10154
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STATE: N'
COUNTRY:
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                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: Proinsulin Peptide Compounds for Detecting TITLE OF INVENTON: and Treating Type I Diabetes NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS: ADDRESSE: LAHIVE & COCKFIELD STRET: 60 State Street, suite 510
CITY: Boston
STATE: Massachusetts
COUNTRY: USA
                                                                                                                                                                             ;
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                                                                                                                                            Length 17;
                                                                                                                                                                           0; Indels
                                                                                                                                       Query Match 100.0%; Score 74; DB 3; I
Best Local Similarity 100.0%; Pred. No. 1.4e-07;
Matches 15; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: DECONI, GIULIO A., Jr.
REGISTRATION NUMBER: 31,503
REFERENCE/POCKET NUMBER: DCI-092PC
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617)227-7400
TELEFAX: (617)227-5941
INFORMATION FOR SEQ ID NO: 23:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: U.S.A.

2.1P: 0210-1875
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: ASCII Text
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08596
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/272,220
FILING DATE: 08-JULY-1994
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                  RESULT 11
PCT-US95-08596-23
Sequence 23, Application PC/TUS9508596
SHORERAL INFORMATION:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 17 amino acids
TYPE: amino acid
TOPOLOGY: linear
                    17 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: peptide
FRAGMENT TYPE: internal
                                                TOPOLOGY: linear

MOLECULE TYPE: peptide

US-09-100-409A-40
                                                                                                                                                                                                             1 OYIKANSKFIGITEL 15
                                                                                                                                                                                                                               3 OYIKANSKFIGITEL 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   amino acid
3Y: linear
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                  LENGTH:
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RESULT 12 PCT-US95-13841-7

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Sequence 13, Application US/08446692
Patent No. 575951
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Zamb, Timothy
TITLE OF INVENTION: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines NUMBER OF SEQUENCES: 114
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
APPLICANT: United Biomedical Inc; Walfield, Alan M.;
APPLICANT: United Biomedical Inc; Walfield, Alan M.;
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: Synthetic IgE Membrane Anchor
TITLE OF INVENTION: Peptide Immunogens for the Treatment of Allergy
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 74; DB 5; I
ilarity 100.0%; Pred. No. 1.4e-07;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Ploppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION UNMBER: PCT/US95/13841
FILING DATE: 25-OCT-1995
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1151-4117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/328,519
FILING DATE: 25-0CT-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Lin, Maria C.H.
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-411
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAM: 212-758-4800
TELEFAM: 212-758-6849
TELEFAM: 421792
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 17 amino acids
                                                                                                                                                     E: Maria C.H. Lin
345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Maria C.H. Lin STREET: 345 Park Avenue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: peptide
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Gaps
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                                                                                                                                                                                                                                                                                                                      100.0%; Score 74; DB 2; Length 27; 100.0%; Pred. No. 2.3e-07; Live 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30B
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            100.0%; Score 74; DB 5; ilarity 100.0%; Pred. No. 2.7e-07; Conservative 0; Mismatches 0;
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 1151-4146 US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212)415-8745
TELEFAX: (516)751-6849
INFORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PCT-US93-11703-63
; Sequence 63, Application PC/TUS9311703
; GENERAL INFORMATION:
APPLICANT: Chiron Mimotopes Pty. Ltd.
TITLE OF INVENTION: T-Cell Epitopes
NUMBER OF SEQUENCES: 75
; CORRESPONDENCE ADDRESS:
ADDRESSE: Grant D. Green
STREET: Emeryville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: PCT/US93/11703
FILING DATE: 28-DEC-1993
CLASSIPICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/984,852
FILING DATE: 02-DEC-1992
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Green, Grant D.
REGISTRATION NUMBER: 31,259
REGISTRATION NUMBER: 0222.101
TELECOMMUNICATION INFORMATION:
TELECHONE: 510-601-2706
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: 510-601-270
TELEFAX: 510-655-3542
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 31 amino acids
                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                           Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
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                                                                                                                                                                                      ; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-488-351A-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 QYIKANSKFIGITEL 15
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 13, Application US/08488351A
Patent No. 5843446
GENERAL INFORMATION:
APPLICANT: Ladd, Anna
APPLICANT: Wang, Chang Yi
APPLICANT: Wang, Chang Yi
APPLICANT: Immunogenic LHRH peptide constructs
TITLE OF INVENTION: and synthetic universal immune stimulators for vaccines
NUMBER OF SEQUENCES. 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,351A
FILING DATE: 7-JUN-1995
CLASSIFICATION: 424
                                          CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/446,692

FILING DATE: 7-JUN-1995

CLASSIETCATION: 424

ATTORNEY/AGENT INFORMATION:

NAME: Maria C.H. Lin

REGISTRATION NUMBER: 29,323

REFERENCE/DOCKET NUMBER: 1151-4146 US2

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212)415-8745

INFORMATION FOR SEQ ID NO: 13:

SEQUENCE CHARACTERISTICS:

TEMPORMATION FOR SEQ ID NO: 13:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 74; DB 1; I
100.0%; Pred. No. 2.3e-07;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION 143.

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/446,692
FILING DATE: 7-00N-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/229,275
FILING DATE: 14-APR-1994
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
CLASSIFICATION: 424
CLASSIFICATION: 424
APPLICATION NUMBER: US 08/057,166
FILING DATE: 27-APR-1992
       COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: Maria C.H. Lin
STREET: 345 Park Avenue
CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATTORNEY/AGENT INFORMATION:
NAME: Maria C.H. Lin
                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 27 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 15; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                             ; MOLECULE TYPE: peptide US-08-446-692-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 QYIKANSKFIGITEL 15
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                                                                                                                                                                                                                                                                                                                                                                                                                            linear
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US-08-488-351A-13
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δ

us-09-763-397a-24.rai

Search completed: January 29, 2002, 10:59:58 Job time: 2144 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

January 29, 2002, 11:00:40; Search time 34.94 Seconds Run on:

(without alignments) 32.702 Million cell updates/sec

US-09-763-397A-24 Perfect score: Sequence:

BLOSUM62 Gapop 10.0 , Gapext 0.5 1 QYIKANSKFIGITEL 15 Scoring table:

219241 segs, 76174552 residues Searched:

219241 Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

piri:* pir2:* pir3:* PIR_68:* Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

	Description	tentoxylysin (EC 3	class II histocomp	qene 84 protein -		hypothetical prote			major merozoite su	major merozoite su	major merozoite su	major merozoite su	blastopia polyprot	Iq heavy chain V-D	hypothetical prote	class II histocomp	hypothetical prote	[acyl-carrier-prot	oligopeptidase (EC	oligoendopeptidase	hypothetical prote		Ig heavy chain V r			Ig heavy chain V-D	Ig heavy chain V r	Ig heavy chain V r	enyla	type II restrictio
SUMMARIES	ID	BTCLTN	S29982	S31029	G86826	T42976	S06286	S16752	A54498	A26868	SAZQGM	A45948	S38635	G48677	G36812	S29980	D85794	G64026	A55485	G86840	S46746	PH1491	PH1516	PH1518	PH1519	F48677	PH1494	PH1488	KIYMC	B71808
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di	Query Match	100.0	60.1	59.5	58.1	58.1	57.4	57.4	57.4	57.4	57.4	57.4	26.8	55.4	55.4	54.7	54.1	54.1	54.1	54.1	54.1	52.7	52.7	52.7	52.7	$^{\circ}$	'n	•		52.7
	Score	74	44.5	44	43	43	42.5	42.5	$^{\circ}$	42.5	42.5	42.5	42	41	41	40.5	40	40	40	40	40	39	39	39	39		39	39	39	39
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probable acetyl-Co type IIS restricti	hypothetical prote hypothetical prote hypothetical prote	trianguatione transporter probable hexosyltr	hypothetical prote hypothetical prote	endo-1,4-beta gluc cellulase (EC 3.2.	methyl-accepting c hemagglutinin-neur	MHC class II beta MHC class II beta	II
T43043 F64690	H71875 A64639 F64472	F70361 F71196	T51466 T29127	A86158 T52135	E82395 HNNZ80	150966 151061	151060
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349	188 188 256	287	383 424	501 501	561 572	82 142	247
52.7	51.4	51.4	51.4	51.4	51.4	50.7	50.7
39	8 8 8 6 6 6	388	38	38	38	37.5	37.5
30	335 337 34 37 37 37	35 36	37 38	39 40	41	43 44	45

ALIGNMENTS

BTCLTN toutonilling and a 2, 2, 2, 60, accommon a plant of the state	rentoxylysin (EC 3.4.24.08) precursor - Clostridium tetani	N;Alternate names: tetanus neurotoxin	C;Species: Clostridium tetani	C;Date: 31-Mar-1988 #sequence_revision 31-Mar-1988 #text_change 18-Jun-1999	C; Accession: A25689; A25757; A25194; B25194; A60759; S69348; S09364	R; Eisel, U.; Jarausch, W.; Goretzki, K.; Henschen, A.; Engels, J.; Weller, U	EMBO J. 5, 2495-2502, 1986	A,Title: Tetanus toxin: primary structure, expression in E. coll, and homolog	A; Reference number: A25689; MUID:87053814	A.Accession. A24689
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li, and homology with b J.; Weller, U.; Hudel,

A;Accession: A25689
A;Molecule type: DNA
A;Molecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Rolecule type: DNA
A;Coss.references: GB:X04436; NID:g40769; PIDN:CAA28033.1; PID:g40770
B;Fairweather, N.F.; Lyness, V.A.
Nucleic Acids Res. 14, 7809-7812, 1986
A;Title: The complete nucleotide sequence of tetanus toxin.
A;Reference number: A25757; MUID:g7040747
A;Accession: A25757

A Residues: 1-1315 <FRI>
A; Residues: 1-1315 <FRI>
A; Residues: 1-1315 <FRI>
A; Residues: 1-1315 <FRI>
A; Experimental Source: Strain CN3911

B; Fairweather, N.F.; Lyness, V.A.; Pickard, D.J.; Allen, G.; Thomson, R.O.
J. Bacteriol. 165, 21-27, 1986

A; Reference number: A25194; MUID:86085672

A; Reference number: A25194

A; Reference number: A25194

A; Reference number: A31194

A; Reference number: A31194

A; Residues: 743-1315

A; Residues: GB:MI2739; NID:9144920; PIDN:AAA23282.1; PID:9144921

A;Accession: B22194
A;Rocession: B22194
A;Rocession: B22194
A;Rocession: B22194
A;Rocession: B22194
A;Rocession: B22194
A;Rocession: B22194
A;Reference number: A60759; MUID: 90035436
A;Reference number: A60759; MUID: 90035436
A;Accession: A60759; MUID: 90035436

G. A; Molecule type: protein
A; Residues: 461-475 <MAT>
R; Residues: 461-475 <MAT>
R; Demotz, S.; Lanzavecchia, L.; Eisel, U.; Niemann, H.; Widmann, C.; Corradin, J. Immunol. 142, 394-402, 1989
A; Title: Delineation of several DR-restricted tetanus toxin T cell epitopes.
A; Reference number: JS0098; MUID:89093918
A; Contents: annotation; epitope region

Rischiavo, C.; Benfenati, F.; Poulain, B.; Rossetto, O.; de Laureto, P.P.; DasGupta, Nature 359, 832-835, 1992
A;Title: Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteo A;Reference number: S27125; MUID:93063293
A;Contents: annotation

```
diamine N-acetyltransferase (EC 2.3.1.57) [imported] - Lactococcus lactis subsp. lact N;Alternate names: spermidine acetyltransferase C;Species: Lactococcus lactis subsp. lactis C;Species: 23-Mar-2001 #sequence_revision 23-Mar-2001 #sequence_revision 23-Mar-2001
A;Cross-references: EMBL:218946; NID:915859; PIDN:CAA79460.1; PID:e59702; PID:9579152 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1992 C;Genetics: A;Gene: 84 A;Start codon: GTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R.Bolotin, A.; Wincker, P.; Mauger, S.; Jaillon, O.; Malarme, K.; Weissenbach, J.; Genome Res. in press, 2001
A,Tille: The complete genome sequence of the lactic acid bacterium.
A,Reference number: A86625
A,Reference number: G86826
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-180 (STO)
A;Residues: 1-180 (STO)
A;Cross-references: GB:AE005176; NID:g12724622; PIDN:AAK05713.1; GSPDB:GN00146
A;Experimental source: strain IL1403
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21-Jan-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C;Species: ateline herpesvirus 3
A;Variety: strain 73 herpesvirus 3
A;Variety: strain 73 herpesvirus 3
A;Variety: strain 74090 #sequence_revision 21-Jan-2000 #text_change : C;Accession: 740976
B;Albrecht, J.C.; Fleckenstein, B.
B;Albrecht, J.C.; Fleckenstein, B.
A;Description: Primary structure of the herpesvirus ateles genome A;Reference number: 222274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 899;
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A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DB 2;
1.9;
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A;Experimental source: strain 73
                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                            0.45;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 43; DB Pred. No. 9.9;
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Pred. No.
                                                                                                                                                                                                                   Score 44;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Gene: yqfF
C;Keywords: acyltransferase; coenzyme A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            58.1%;
69.2%;
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ilarity 64.3%;
Conservative
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ilarity 57.1%;
Conservative
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65 ||EANDTFIGIVEL 77
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Best Local Similarity
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A; Residues: 1-899 <ALB>
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Matches 9; Conserv
                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
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R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
R;Donnelly-Wu, M.K.; Jacobs Jr., W.R.; Hatfull, G.F.
Mol. Microbiol. 7, 407-417, 1993
A;Title: Superinfection immunity of mycobacteriophage L5: applications for genetic trans
A;Reference number: S30949; MUID:93211283
A;Accession: S31029
A;Accession: S31029
A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
                                                                                                                                          A; Molecule type: protein
A; Residues: 2-31 < DEE>
C; Comment: The source of this protein was an extrachromosomal plasmid.
C; Comment: The source of this protein was an extrachromosomal plasmid.
C; Comment: The precursor is cleaved by endogenous proteinase activity to form light (fradual chains are not toxic when separated). The amino end of the heavy chain (fragment B) C; Comment: Fragment B forms ion channels in a lipid bilayer. Fragment C binds to ganglic C; Comment: This potent neurotoxin binds to peripheral neuronal synapses, is internalized presynaptic neurons. It inhibits neurotransmitter release by proteolytic cleavage of sy
  R;de Filippis, V.; Vangelista, L.; Schiavo, G.; Tonello, F.; Montecucco, C.
Eur. J. Blochem. 229, 61-69, 1995
A;Title: Structural studies on the zinc-endopeptidase light chain of tetanus neurotoxin.
A;Recession: S69348; MUID:95262688
A;Accession: S69348
                                                                                                                                                                                                                                                                                                                                                                                   A; Description: blocks neuroexocytosis via hydrolysis of a Gln-Phe peptide bond in synapt
                                                                                                                                                                                                                                                                                                                                                                                                                C'Superfamily: tetanus toxin
C'Superfamily: tetanus toxin
C'Keywords: hydrolase, metalloproteinase; neurotoxin; transmembrane protein; zinc
C'Keywords: hydrolase; metalloproteinase; neurotoxin; transpectus predicted cTTL>
F.2-457/Product: tentoxylysin heavy chain (fragment B.C) #status experimental cTTH>
F.461-1315/Product: tentoxylysin heavy chain (fragment B.C) #status predicted cTXB>
F.461-864/Domain: channel forming (fragment C) #status predicted cTXB>
F.865-1315/Domain: ganglioside binding (fragment C) #status predicted cTXC>
F.233,237/Binding site: zinc (His) #status predicted
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C;Species: Salmo salar (Atlantic salmon)
C;Species: Salmo salar (Atlantic salmon)
C;Species: S2982
R;Hordvik, I.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S29980
A;Accession: S2992
A;Accession: S2991
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C;Species: Mycobacterium phage L5
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 08-Oct-1999
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A;Residues: 1-244 CHOR>
A;Cross-references: EMBL:X70166; NID:g64369; PID:g64370
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
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100.0%; Pred. No. 2.8e-05;
Live 0; Mismatches 0;
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55.6%;
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Best Local Similarity 100.
Matches 15; Conservative
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Best Local Similarity
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major merozoite surface antigen precursor - malaria parasite (Plasmodium falciparum)
N.Alternate names: 195K glycoprotein
C.Species: Plasmodium falciparum
C.Species: A23386; S06361
R.Weber, J.L.; Lahinger, W.M.; Lyon, J.A.
Nucleic Acids Res: 14, 3311-3323, 1986
A; Title: Variation in the gene encoding a major merozoite surface antigen of the huma A; Reference number: A23386; MUID:86205236
A; Molecule type: DNA
A; Molecule typ
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C;Comment: The merozoite stages of different strains have strain-specific surface ant
C;Comment: P. falciparum has three stages: sporozoite, merozoite, and gametocyte. The
C;Superfamily: major merozoite surface antigen
C;Superfamily: major merozoite; surface antigen; tandem repeat
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C;Superfamily: major merozoite surface antigen
C;Keywords: surface antigen
C;Keywords: surface antigen
E;1-19/Domain: signal sequence #status predicted <SIG>
F;20-1701/Product: major merozoite surface antigen #status predicted <MAT>
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                                           A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-1701 <PET>
A;Cross-references: GB:M19143; NID:g160412; PIDN:AAA29653.1; PID:g160413
C;Superfamily: major merozoite surface antigen
C;Keywords: Surface antigen
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A;Accession: A26868
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Pred. No. 23;
4; Mismatches
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1001 QFVKSNSKVITGLTE 1015
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A; Residues: 1104-1726 <WEB2>
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Best Local Similarity
Matches 9; Conserv
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             A; Accession: A54498
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                                                                                                                                                                                                 major merozolte surface antigen precursor - malaria parasite (Plasmodium falciparum) (st Ni Alternate names: 190K protein; polymorphic schizont antigen ("Species: Plasmodium falciparum ("Species: 13-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 09-Jun-2000 ("Species: 10: Matile, H.; Reber-Liske, R. EMBO J. 6, 4137-4142, 1987 ("Attle: A naturally occurring gene encoding the major surface antigen precursor pl90 of A; Reference number: S06286 ("MUD:88166657 A; Reference number: S06286 A; Status: not compared with conceptual translation A; Molecule type: DNA A; Molecule type: DNA A; Residues: 1-1060 <CER> C; Superfamily: major merozoite surface antigen ("Keywords: surface antigen
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Pred. No. 15;
4; Mismatches
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Pred. No. 14;
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1009 QFVKSNSKVITGLTE 1023
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983 QFVKSNSKVITGLTE 997
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124 QYITSNSTFTGQTE 137
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Best Local Similarity
Matches 9; Conserv
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C; Superfamily
C; Keywords: q
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Ig heavy chain V-D-J region (419.1) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 17-Mar-1999
C;Accession: G48677
R;Tassignon, J.; Brait, M.; Jamila, I.; Urbain, J.; Gottlieb, P.; Brown, A.; Hasemann Proc. Natl. Acad. Sci. U.S.A. 90, 9508-9512, 1993
A;Title: Molecular characterization of monoclonal CRI-A-positive anti-arsonate antibo A;Accession: G48677; MUID:94022404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          S29980
class II histocompatibility antigen - Atlantic salmon
C;Species: Salmo salar (Atlantic salmon)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C;Accession: S29980
R:Hordvik, I.
Submitted to the EMBL Data Library, October 1992
A;Reference number: S29980
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Species: saimiriine herpesvirus 1
A;Note: host Saimiri sciureus (common squirrel monkey)
C;Date: 16-Oct-1992 #sequence_revision 16-Oct-1992 #text_change 08-Oct-1999
C;Accession: G36812
R;Albrecht, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Submitted to the EMBL Data Library, January 1992
A; Description: Primary structure of the herpesvirus saimiri genome.
A; Reference number: A56806
A; Accession: G36812
A; Molecule type: DNA
A; Residues: 1-899 Aclab
A; Cross-references: GB:X64346; NID:g60320; PIDN:CAA45686.1; PID:g60384
B; Albrecht, J.C.; Nicholas, J.; Biller, D.; Cameron, K.R.; Biesinger, B.; N. Virol. 66, 5047-5058, 1992
A; Tile: Primary structure of the herpesvirus saimiri genome.
A; Reference number: A37309; MUID:9233588
A; Contents: annotation; protein-coding frames
A; Note: neither protein nor nucleotide sequence is given
C; Genetics:
A; Gene: 63
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         - saimiriine herpesvirus 1 (strain 11)
                                                                                                                                                                                                                                                                   A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                  C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin F;15-98/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 123;
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124 QYITSNATFIGLSE 137
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Best Local Similarity
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Matches 7
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                  F;20-1726/Product: major merozoite surface antigen #status predicted <MAT>
F;67-87,91-96,100-105,109-120/Region: 3-residue repeats (S-G-T)
F;757-765/Region: 3-residue repeats (T-E-E)
F;133,272,501,567,638,827,839,924,944,990,1016,1114,1221,1613,1658/Binding site: carbohy
                                                                                                                                                                                                                                                                                                                                                                                                                  C; Species: Plasmodium falciparum
C; Species: Plasmodium falciparum
C; Obate: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jun-2000
C; Accession: A45948
R; Chang, S.P.; Kramer, K.J.; Yamaga, K.M.; Kato, A.; Case, S.E.; Siddiqui, W.A.
Exp. Parasitol. 67, 1-11, 1988
A; Title: Plasmodium falciparum: gene structure and hydropathy profile of the major meroz
A; Reference number: A45948; MUID:89005525
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C;Species: Drosophila melanogaster
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 17-Nov-2000
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A; Residues: 1-1333 <FRO>
A; Cross-references: EMBL:Z27119; NID:g415797; PID:g415798
F;1-19/Domain: signal sequence #status predicted <SIG>
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Pred. No. 23;
3; Mismatches
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                                                                                                                                                                               Pred. No. 24;
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A; Residues: 1-1726 <CHA>
A; Cross-references: GB: M37213
Cs. Superfamily: major merozoite surface antigen
C; Keywords: surface antigen
                                                                                                                                                        Score 42.5;
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C;Keywords: polyprotein
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1026 QFVKSNSKVITGLTE 1040
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1026 QFVKSNSKVITGLTE 1040
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Best Local Similarity 60.0
Matches 9; Conservative
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Best Local Similarity
Local 9; Conserve
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A; Cross-references: FlyBa
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Best Local Similarity
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B.; Newman, C.;

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A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-245 *COPA
A;Cross-references: EMBL:X70167; NID:964371; PID:964372
C;Superfamily: class II histocompatibility antigen; immunoglobulin homology
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Gaps Query Match
Best Local Similarity 44.4%; Pred. No. 7.6;
Matches 8; Conservative 5; Mismatches 2; Indels

1 OYIKANS---KFIGITEL 15 :|::|| |::||| 53 EYVRFNSTVGKYVGYTEL 70 Q ò

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"Tetanus toxin is a zinc protein and its inhibition of neurotransmitter release and protease activity depend on zinc.";
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"Limited proteolysis of tetenus toxin. Relation to activity and
identification of cleavage sites.";
Eur. J. Biochem. 202:41-51(1991).
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IDEMTIFICATION AS ZINC-PROTEASE.
MEDLINE-93010948; PubMed-1396558;
Schlavo G., Poulain B., Rossetto O., Benfenati F., Tauc L.,
Montecucco C.;
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Copyright (c) 1993 - 2000 Compugen Ltd.
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GNT1_HUMAN
GNT1_MOUSE
GNT1_RABIT
GNT1_RAT
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G6PD_ASPNG
G6PD_EMENI
YDDS_SCHPO
YJSS_BUCAI
MIP_CHLPN
YDO1_CLOAB
DPOB_XENLA
MURD_BACSU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        YHJ9_YEAST
KAD_MYCCA
YD83_METJA
TRUB_AQUAE
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Y032_BORBU
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G6PD_PICJA
YND1_YEAST
                                                                                                                                      January 29, 2002, 11:16:19
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Maximum Match 100%
Listing first 45 summaries
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                                                                                          OM protein - protein search, using sw model
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Gapop 10.0 , Gapext 0.5
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74
1 QYIKANSKFIGITEL 15
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Maximum DB seq length: 200000000
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RESULT 3
MSP1_PLAF3
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                                                                                                                                                                                                                  neurotoxin.";
Nat. Struct. Biol. 4:788-792(1997).
Nat. Struct. Biol. 4:788-792(1997).
-!- FUNCTION: TETANUS TOXIN ACTS BY INHIBITING NEUROTRANSMITTER
RELEASE. IT BINDS TO PERIPHERAL NEURONAL SYNAPSES, IS INTERNALIZED
AND MOWES BY RETROGRADE TRANSPORT UP THE AXON INTO THE SPINAL CORD
WHERE IT CAN MOVE BETWEEN POSTSYNAPTIC AND PRESYNAPTIC NEURONS. IT
INHIBITS NEUROTRANSMITTER RELEASE BY ACTING AS A ZINC
ENDOPPETIDASE THAT CATALYZES THE HYDROLYSIS OF THE 76-GLN-|-PHE-777
                                                                                                                                                                                                                                                                                                                                                                                SUBUNIT: THE PRECURSOR POLYPEPTIDE IS SUBSEQUENTLY CLEAVED TO YIELD SUBCHAINS L AND H. THESE REMAIN LINKED BY A DISULFIDE BRIDGE AND ARE NON-TOXIC AFTER SEPARATION.

MISCELLANEOUS: THE C-TERMINAL OF THE HEAVY CHAIN BINDS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                          GANGLIOSIDE RECEPTORS.
SIMILARITY: BELONGS TO PEPTIDASE FAMILY M27 (ZINC
METALLOPROTEASE); ALSO KNOWN AS THE TETANUS/BOTULINUM NEUROTOXIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hydrolase; Metalloprotease; Zinc; Plasmid;
                                                                                                                                                           MEDLINE=97475217; PubMed=9334741;
Umland T.C., Wingert L.M., Swaminathan S., Furey W.F., Schmidt J.J.,
Sax M.;
                                                       Schiavo G., Benfenati F., Poulain B., Rossetto O., de Laureto P.P., Dasgupta B.R., Montecucco C.; "Tetanus and botulinum-B neurotoxins block neurotransmitter release by proteolytic cleavage of synaptobrevin.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZINC (CATALYTIC) (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                       BOND OF SYNAPTOBREVIN-2. CATALYTIC ACTIVITY: HYDROLYSIS OF 76-GLN-1-PHE-77 BOND IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZINC (CATALYTIC) (BY SIMILARITY).
POTENTIAL.
                                                                                                                                                                                                      "Structure of the receptor binding fragment HC of tetanus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MW; 134C3657133EF81D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TETANUS TOXIN LIGHT CHAIN. TETANUS TOXIN HEAVY CHAIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CHAIN
                                                                                                                                              X-RAY CRYSTALLOGRAPHY (2.7 ANGSTROMS) OF 874-1314.
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InterPro; IPR000130; Zn_MTpeptdse.
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                                          MEDLINE-93063293; PubMed-1331807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF01742; Peptidase_M27; 1.
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EMBL; M12739; AAA23282.1; --
EMBL; X06214; CAA29564.1; --
PIR; A25689; BTCLTN.
PDB; 1AF9; 29-APR-98.
PDB; 1A8D; 14-OCT-98.
MEROPS; M27.001; --
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       150550
                             IDENTIFICATION OF SUBSTRATE
3MBO J. 11:3577-3583(1992)
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1092
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                                                                                                                                                                                                                                                                                                                                                                       SYNAPTOBREVIN.
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INIT_MET
CHAIN
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Length 1314;

Score 74; DB 1; Pred. No. 1.3e-05;

100.0%;

Query Match Best Local Similarity

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                                                                                                                                                                                                                                                                                                                                                                                                                                           "DNA sequence, structure and gene expression of mycobacteriophage L5:
a phage system for mycobacterial genetics.";
Mol. Microbiol. 7:395-405(1993).
   Gaps
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MEDLINE=8816657; PubMed=3327688;
Certu U., Rotmann D., Matile H., Reber-Liske R.;
"A naturally occurring gene encoding the major surface antigen precursor pl90 of Plasmodium falciparum lacks tripeptide repeats.";
EMBO J. 6:4137-4142(1987).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MSPI_PLAF3 STANDARD; PRT; 1682 AA.
P19598; Q25921;
01-FEB-1991 (Rel. 17, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
01-NOV-1997 (Rel. 35, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                       Viruses; dsDNA viruses, no RNA stage; Tailed phages; Siphoviridae.
NCBL_TaxID=31757;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 44; DB 1; Length 66; Pred. No. 0.2;
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                                                                                                                                                                                                           (Rel. 28, Created)
(Rel. 28, Last sequence update)
(Rel. 28, Last annotation update)
                                                                                                                                                                           66 AA.
   Mismatches
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                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A. MEDLINE-9311182; PubMed-8459766; Hatfull G.F., Sarkis G.J.; "DNA sequence, structure and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE OF 1032-1682 FROM N.A. MEDLINE=95354793; PubMed=7628566; Tolle R., Bujard H., Cooper J.A.;
 ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; Z18946; CAA79460.1; -. PIR; S31029; S31029.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         59.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   7424 MW;
 Conservative
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                                                                                                                                                                           STANDARD;
                                     1 QYIKANSKFIGITEL 15
                                                                                                                                                                                                                                                                       GENE 84 PROTEIN (GP84).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         63
                                                             829 QYIKANSKFIGITEL
                                                                                                                                                                                                                                                                                                             Mycobacteriophage L5.
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66 AA; 7
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nes 8; Conserv
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NCBI_TaxID=5834;
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                                                                                                                                                                       VG84_BPML5
Q05301;
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01-FEB-1994
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15;
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(POTENTIAL)
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                                                                                                                                                                                                          Transmembrane;
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P08569;
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                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                         42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A. MEDIA, SEQUENCE FROM N.A. MEDIA, SEQUENCE FROM N.A. MEDIA, SEQUENCE M.G., Coppel R.L., McIntyre P., Langford C.J., Woodrow G., Brown G.V., Anders R.F., Kemp D.J., "Variation in the precursor to the major merozoite surface antigens of Plasmodium falciparum.", 27:291-302(1988).
                                                                    OF.
         merozoite surface antigen-1.";
Exp. Parasitol. 81:47-54(1995).
-!- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
'Plasmodium falciparum: variations within the C-terminal region of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOL. Biochem. Parasitol. 27:291-302(1988).
-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                        83 KDA,
                                                     -i- PTM: MEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA
KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS
MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                                                                                                                                                                                                                                                                                                                                           (POTENTIAL).
(POTENTIAL).
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Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
Transmembrane; GPI-anchor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 42.5; DB 1; Length 1682; Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         глаsmodium falciparum (isolate FC27 / Papua New Guinea).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_ТахID-5837;
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N-LINKED (GLCNAC...)
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EMBL; X00087; CAA66280.1; -.
EMBL; Z35326; CAA84555.1; -.
PIR; S06286; S06286
InterPro; IPRO00561; EGF-11ke.
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                                            (POTENTIAL).
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P13819;
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Tanabe K., Mackay M., Goman M., Scaife J.G.;
"Allelic dimorphism in a surface antigen gene of the malaria parasite
Placemodium falcinarum ".
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PTM: MEROZÓTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
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InterPro; IPRO000561; EGF-11ke.
Pfam; PF000008; EGF; I.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_TaxID=70153;
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SEQUENCE OF 1-115 FROM N.A.
MEDLINE-86136024; PubMed=3004972;
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J. Mol. Biol. 195:273-287(1987).
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MEDLINE-86205236; PubMed=3517809;
Weber J.L., Leininger W.M., Lyon J.A.;
"Variation in the gene encoding a major merozoite surface antigen of
the human malaria parasite Plasmodium falciparum.";
Nucleic Acids Res. 14:3311-3323(1986).
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01-OCT-1996 (Rel. 34, Last annotation update)
MEROZOITE SURFACE PROTEIN 1 PRECURSOR (MEROZOITE SURFACE ANTIGENS)
                                                                                                     EMBO J. 4:3823-3829(1985).
                                                                                                                                                                            KDA,
Mackay M., Goman M., Bone N., Hyde J.E., Scaife J., Certa U., Stunenberg H., Bujard H.; 
*Stunenberg H., Bujard H.; 
*Polymorphism of the precursor for the major surface antigens of Plasmodium falciparum merozoites: studies at the genetic level.";
                                                                                                                                                                       -!- PTM: MERCACITE SURPACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS MERCACOLIES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
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Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
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                                                                                                                                                                                                           42
                                                 R.\,; the Camp strain of the human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Plasmodium falciparum: gene structure and hydropathy profile of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                   Q
                   MEDLINE-80143999; PubMed-3278296; Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.; Weber J.L., Sim B.K.L., Lyon J.A., Wolff R.; Merozoite surface protein sequence from the Camp strain of the hum malaria parasite Plasmodium falciparum."; Nucleic Acids Res. 16:1206-1206(1988).

-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-0cT-1996 (Rel. 34, Created)
01-0cT-1996 (Rel. 34, Last sequence update)
01-0cT-1996 (Rel. 34, Last unocation update)
MEROZOLIE SURFACE PROTEIN 1 PRECURSOR (MEROZOLIE SURFACE ANTIGENS)
                                                                                                                                                                                                     -i- PTM: WEROZÓITE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Interpro; IPR000561; EGF-like.
Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (POTENTIAL)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Plasmodium falciparum (isolate Palo Alto / Uganda).
Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-89005225; Pubmed-3049134;
Chang S.P., Kramer K.J., Yamaga K.M., Kato A., Case S.E.,
Siddiqui W.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEROZOITE SURFACE PROTEIN 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-LINKED GLCNAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1726 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 42.5;
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OF 1104-1726 FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PIR; A23386; SAZQGM.
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NCBI_TaxID=57270;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (PMMSA) (GP195).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Transmembrane;
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P50495;
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SIMILARITY)
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Q01055;
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SEQUENCE
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                                                     42
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1- COPACTOR: THIS ENZYME TIGHTLY BINDS ONE ZINC ATOM PER CHAIN WHICH IS REQUIRED FOR THE CATALYTIC MECHANISM. IT ALSO BINDS WEAKLY TO TWO OTHERS ZINCS WHICH ARE NOT ESSENTIAL FOR ACTIVITY (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps
                                                  PTM: MEROZOTTE SURFACE ANTIGEN CONTAIN THE SEQUENCE OF 83 KDA, 4 KDA AND 19 KDA ANTIGENS WHICH ARE THE MAJOR SURFACE ANTIGENS OF MEROZOITES. THE MATURATION TAKE PLACE DURING SCHIZONT.
                    exp. Parasitol. 67:1-11(1988).
-1- SUBCELLULAR LOCATION: ATTACHED TO THE MEMBRANE BY A GPI-ANCHOR
                                                                                                                                                                                                                                                                                                                                                    (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Berkmen M., Benedik M.J.;
"Din Inhibits transcription of Serratia marcescens nuclease.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases.
-!- CATALYTIC ACTIVITY: DIHYDROOROTATE + H(2)0 = N-CARBAMOYL-
major merozoite surface antigen (gp195) of the Uganda-Palo Alto
                                                                                                                                                                                                                                                                                                                               (POTENTIAL)
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Pfam; PF00008; EGF; 1.
Malaria; Merozoite; Polyprotein; Repeat; Signal; Glycoprotein;
                                                                                                                                                                                                                                                                           POTENTIAL
                                                                                                                                                                                                                                                                                                                                                                                                                                           Length 1726;
                                                                                                                                                                                                                                                                                                                                                                                                                                                               1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                          5B59CEEFA2F9A026 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 42.5; DB 1;
Pred. No. 11;
4; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
DIHYDROOROTASE (EC 3.5.2.3) (DHOASE) (FRAGMENT).
                                                                                                                                                                                                                                                    MEROZOITE SURFACE
N-LINKED (GLCNAC.
N-LINKED (GLCNAC.
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20-AUG-2001 (Rel. 40, Last seq
20-AUG-2001 (Rel. 40, Last anno
                                                                                                                                                                                                                                                                                                                                                                                                                                          57.4%;
60.0%;
                                                                                                                                                                                     EMBL; M37213; AAA29611.1; -
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1026 QFVKSNSKVITGLTE 1040
                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 60.0°
                                                                                                                                                                                                                             Transmembrane, GPI-anchor
SIGNAL 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 QYIKANSKFI-GITE 14
                                                                                                                                                                                                                                                                                                                                                                      1221 122
1613 161
1726 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serratia marcescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                           (POTENTIAL).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=615;
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Q9S3S1;
                                                                                                                                                                                                                                                              CARBOHYD
CARBOHYD
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            solate
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
-1- PATHWAY: THIRD STEP IN PYRIMIDINE BIOSYNTHESIS.
-1- SUBUNIT: HOMODIMER (BY SIMILARITY).
-1- SIMILARITY: BELONGS TO THE DHOASE FAMILY. SUBFAMILY 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE=9233588; PubMed=1321287;
Albrecht J.-C., Nicholas J., Biller D., Cameron K.R., Blesinger B., Newman C., Wittmann S., Craxton M.A., Coleman H., Fleckenstein B., Honess R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organization between HVS and Epstéin-Barr virus.";
Virology 188:296-310(1992).
-!- SIMILARITY: BELONGS TO FAMILY THAT GROUPS TOGETHER HSV-1 UL37,
EHV-1 23, EBV BOLFI, VZV 21, HVS-1 63, AND HCMV UL47.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nicholas J., Cameron K.R., Coleman H., Newman C., Honess R.W.; "Analysis of nucleotide sequence of the rightmost 43 kbp of herpesvirus saimiri (HVS) L-DNA: general conservation of genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        55.4%; Score 41; DB 1; Length 204; 46.2%; Pred. No. 2.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     204 AA; 22899 MW; 9DB0B6C9B834B310 CRC64;
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J. Virol. 66:5047-5058(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Viruses; dsDNA viruses, no RNA stage; Herpesviridae;
Gammaherpesvirinae; Rhadinovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-APR-1993 (Rel. 25, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
CAPSID ASSEMBLY PROTEIN 63.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF175466; AAD50307.1; ALT_INIT.
INTERPO; IPR002195; Dihydrocratase.
PROSITE: PS00482; DIHYDROCROTASE_1; PARTIAL.
PROSITE; PS00483; DIHYDROCROTASE_2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pyrimidine biosynthesis; Hydrolase; Zinc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 or send an email to license@isb-sib.ch).
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MEDLINE-92230228; Pubmed-1314457;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Herpesvirus saimiri (strain 11).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Best Local Similarity 46.2
Matches 6; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | | | : : | : : | : | | | 42 QYVQAGNRFLGAT
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Length 194;

9

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Query Match
                                                                                                     RESULT 11
PEF1_LACLC
                      Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Whole-genome random sequencing and assembly of Haemophilus influenzae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAINED / KW20 / ATCC 51907;
MEDLINE-95550630; PubMed=7542800;
RELischmann R.D., Adams M.D., White O., Clayton R.A., Kirkness E.F., Kerlavage A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L. I., Glodek A., Kelley J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Eine L.D., Fritchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                                                                               "Characterization of the Haemophilus influenzae topA locus: DNA topoisomerase I is required for genetic competence."; Gene 169:25-31(1996).
                                                                                 .;
0
                                                                                                                                                                                                                                                                    Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                         01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ACYL CARRIER PROTEIN PHOSPHODIESTERASE (EC 3.1.4.14) (ACPPROSPHOLESTERASE)
                                                          Length 899
                                                                                 Indels
PIR; G36812; G36812.
Capsid assembly.
SEQUENCE 899 Aa; 103350 MW; F1429B3770A2885E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A8AEC9D00829522C CRC64;
                                                         Score 41; DB 1;
Pred. No. 11;
                                                                                                                                                                                     194 AA.
                                                                                 4; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      or send an email to license@isb-sib.ch).
                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                                                                                              STRAIN=RD / KW20 / ATCC 51907;
MEDLINE=96186898; PubMed=8635745;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TIGR; HI1366; -.
Hydrolase; Complete proteome.
SFOUENCE 194 AA; 21208 MW;
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                                                          55.4%;
                                                                                                                                                                                                                                                                                                                                                                       Chandler M.S., Smith R.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Science 269:496-512(1995).
                                               Query Match
Best Local Similarity 5v.v.
7; Conservative
                                                                                                                                                                                    STANDARD;
                                                                                                                              124 OYITSNATFIGLSE 137
                                                                                                       1 QYIKANSKFIGITE 14
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SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=727;
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"Duplication of the pepF gene and shuffling of DNA fragments on the "Duplication of the pepF gene and shuffling of DNA fragments on the lactose plasmid of Lactosoccus lactis.";
J. Bacteriol. 179:4164-417(1997).
-i. FUNCTION: HYDROLYZES PEPTIDES CONTAINING BETWEEN 7 AND 17 AMINO ACIDS WITH A RATHER WIDE SPECIFICATY.
-i. COFACTOR: BINDS ONE ZINC ION (BY SIMILARITY).
-i. SIMILARITY: BELONGS TO PEPTIDASE FAMILY M3 (ZINC METALLOPROTEASE);
ALSO KNOWN AS THE THIMET OLIGOPEPTIDASE SUBFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-55096044; PubMed-7798200;
Monnet V., Nardi M., Chopin A., Chopin M.-C., Gripon J.-C.;
"Biochemical and genetic characterization of PepF, an oligopeptidase
                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            or send a..

EMBL; X3252; CAA6333.1;

MEROPS; M03.007; -0..

A MEROPS; M03.007; -0..

MICAFPO; IPR001567; Peptidase_M3.

DR PADM; PF01432; Peptidase_M3.

DR PROSITE; PS00142; ZINC_PROTEASE; FALSE_NEG.

MW Hydrolase; Metalloprotease; Zinc; Plasmid.

"" SITE 388 388 BY SIMILARITY).

394 ZINC (CATALYTIC) (BY SIMILARITY).

394 ZINC (CATALYTIC) (BY SIMILARITY).

"" SITE 388 SIN SIMILARITY).

"" SITE 388 SIN SIMILARITY).

"" CAPALYTIC) (BY SIMILARITY).

"" SITE 394 ZINC (CATALYTIC) (BY SIMILARITY).

"" CABSCSIGFFAZET 87 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;
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                                                               Indels
Score 40; DB 1;
Pred. No. 3.3;
                                                                                                                                                                                                                                                                                                                                               PEFI_LACLC STANDARD; PRT; 601 AA. P54124; P94880; 01-0CT-1996 (Rel. 34, Created) 01-0CT-1996 (Rel. 34, Last sequence update) 01-0CT-010G (Rel. 40, Last annotation update) 0LIGOENDOPEPTIDASE F, PLASMID (EC 3.4.24.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ed. No. 11;
Mismatches
                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A., AND PARTIAL SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 om Lactococcus jactis.";
Biol. Chem. 269:32070-32076(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN=NCDO 763;
MEDLINE=97352670; PubMed=9209029;
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                                                                   Conservative
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147 QYMKSILGFIGITDV 161
                                                                                                                               1 OYIKANSKFIGITEL 15
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A. STRAIN=NCDO 763;
                                      Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-NCDO 763;
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capricolum.
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                                     Entomoplasmataceae.
                                                                                                                                                                                                                                                                                                                                                S02851; KIYMC
                                                                        SEQUENCE FROM N.A.
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                                                   NCBI_TaxID=2095;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   YD83_METJA
Q58778;
            Mycoplasma
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SEQUENCE
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                                                                                                                                                                                                                                                      STRAIN-S288C / AB972;
MEDLINE-94378003; PubMed-8091229;
Johnston M., Andrews S., Brinkman R., Cooper J., Ding. H., Dover J.,
Johnston M., Andrews S., Brinkman R., Cooper J., Ding. H., Dover J.,
Kucaba T., Hillier L., Jier M., Johnston L., Langston Y.,
Latreille P., Louis E.J., Macri C., Mardis E., Menezes S., Mouser L.,
Nhan M., Rifkin L., Riles L., St Peter H., Trevasis E., Vaughan K.,
Vignati D., Wilcox L., Wohldman P., Waterston R., Wilson R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                      Complete nucleotide sequence of Saccharomyces cerevisiae chromosome
                                                                                                                                                                                 Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fung1; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                              ol-FEB-1995 (Rel. 31, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
HYPOTHETICAL ALDEHYDE-DEHYDROGENASE LIKE PROFEIN IN FIL1-VMA10
INTERGENIC REGION.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ö
                                                                                                                                                                                                                                                                                                                                                                                            Science 265:2077-2082(1994).
-!- SIMILARITY: BELONGS TO THE ALDEHYDE DEHYDROGENASES FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-MAR-1989 (Rel. 10, Created)
01-MAR-1989 (Rel. 10, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
ADENYLATE KINASE (EC 2.7.4.3) (ATP-AMP TRANSPHOSPHORYLASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ore 40; DB 1; Length 644; ed. No. 12; Mismatches 5; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54DADDAEB2A16D4D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BY SIMILARITY.
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00171; aldedh; 1.
PROSITE; PS00070; ALDEHYDE_DEHYDR_CYS; 1.
PROSITE; PS00687; ALDEHYDE_DEHYDR_GLU; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              54.1%; Score 40; 60.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PIR; S46746; S46746.
SGD; S0001081; YHR039C.
InterPro; IPR002086; Aldehyde_dehydr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hypothetical protein; Oxidoreductase.
ACT_SITE 354 354 RV STATE
                                                                                    PRT;
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                                                                                                          01-FEB-1995 (Rel. 31, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            71320 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EMBL; U00062; AAB68915.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9; Conservative
                                                                                    STANDARD;
                       284 RYIELRKKILGITDL 298
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
1 OYIKANSKFIGITEL 15
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Matches 9; Conserv
                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                 YHJ9_YEAST
P38694;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   KAD_MYCCA
P10251;
                                                                                                                                                                                                                                                                                                                                                            Vaudin M.;
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SEQUENCE
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                                                         RESULT 12
YHJ9_YEAST
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Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
Button G.G., Blake J.A., Fitzgerald L.M., Clayton R.A., Gocayne J.D.,
Kerlavage A.R., Dougherty B.A., Tomb J.-F., Adams M.D., Reich C.I.,
Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
Scott J.L., Geoghagen N.S.M., Weidman J.F., Fuhrmann J.L.,
Utterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                        Ohkubo S., Muto A., Kawauchi Y., Yamao F., Osawa S.;
"The ribosomal protein gene cluster of Mycoplasma capricolum.";
Mol. Gen. Genet. 210:314-322(1987).
-!- FUNCTION: THIS SHALL UBIOUTTOUS ENZYME IS ESSENTIAL FOR MAINTENANCE AND CELL GROWTH.
-!- CATALYTIC ACTIVITY: ATP + AMP = ADP + ADP.
-!- SUBUNIT: MONOMER (BY SIMILARITY).
-!- SUBURILALIAR LOCATION: CYTOPLASMIC.
-!- SIMILARITY: BELONGS TO THE ADENYLATE KINASE FAMILY.
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Bacteria; Firmicutes; Bacillus/Clostridium group; Mollicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 213;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ransferase; Kinase; ATP-binding.
PLBIND 7 15 ATP (BY SIMILARITY).
SEQUENCE 213 AA; 24616 MW; FBCFA426B6F92E16 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
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ProDom; PD000657; Adenylate_kin; 1.
PROSITE; PS00113; ADENYLATE_KINASE; 1.
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STRAIN-JAL-1 / DSM 2661 / ATCC 43067;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL PROTEIN MJ1383 PRECURSOR
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InterPro; IPR000850; Adenylate_kin.
Pfam; PF00406; adenylatekinase; 1.
                                                                                                                                                                                       STRAIN=ATCC 27343 / KID;
MEDLINE=88142549; Pubmed=3481422;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ;
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72.78;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 52.7
Best Local Similarity 72.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the Buropean Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
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Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.; "Complete genome sequence of the methanogenic archaeon, Methanococcus jannaschii.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nature 392:353-358(1998).
-!- FUNCTION: FORMATION OF PSEUDOURIDINE AT POSITION 55 IN THE PSI GC LOOP OF TRANSFER RNAS (BY SIMILARITY).
-!- CATALYTIC ACTIVITY: URACIL + D-RIBOSE 5-PHOSPHATE = PSEUDOURIDINE 5'-PHOSPHATE + H(2)0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO THE TRUB FAMILY OF PSEUDOURIDINE SYNTHASES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Deckert G., Warren P.V., Gasterland T., Young W.G., Lenox A.L., Graham D.E., Overbeek R., Snead M.A., Keller M., Aujay M., Huber R., Feldman R.A., Short J.M., Olson G.J., Swanson R.V., "The complete genome of the hyperthermophilic bacterium Aquifex
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
TRNA PSEUDOURIDINE SYNTHASE B (EC 4.2.1.70) (TRNA PSEUDOURIDINE 55
SYNTHASE) (PSI55 SYNTHASE) (PSEUDOURIDYLATE SYNTHASE) (URACIL
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6D26F427EAB54675 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Indels
                                                                                                                                                                                                                                                                               InterPro; IPR001130; UPF0006.
Pfam; PF01026; TatD_DNase; 1.
Hypothetical protein; Signal; Complete proteome. SIGNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Aquifex aeolicus.
Bacteria; Aquificales; Aquificaceae; Aquifex.
NCBL_TaxID=63363;
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                                                                                                                                                                                                                                                                                                                                                                                                                             Score 38; DB :
Pred. No. 10;
3; Mismatches
                                                   Science 273:1058-1073(1996).
-!- SIMILARITY: TO M.JANNASCHII MJ0761.
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                                                                                                                                                                                                                                                                                                                                                                         29036 MW;
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Matches 7; Conservative
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256 AA;
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EMBL; AE000703; AAC06885.1; -. InterPro; IPR002501; Trub_N.

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                                                                Length 287;
                                                                                        Indels
Pfam; PF01509; TruB_N; 1.
Lyase; tRNA processing; Complete proteome.
SEQUENCE 287 AA; 32259 MW; 2E58C1B7CEAD58AA CRC64;
                                                               Score 38; DB 1;
Pred. No. 12;
1; Mismatches
                                                                                                                                                                                    Search completed: January 29, 2002, 11:16:20 Job time: 149 sec
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Best Local Similarity 69.2
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263 IYEDSKFIGIGEL 275
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Title:
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Listing first 45 summaries
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1: sp_archea:*
2: sp_bacteria
3: sp_fungi:*
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108
1 MKELVNVALVEMUTVI
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2000 Compugen Ltd.
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sp_plant:*
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sp_mammal:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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425	379	331	320	137	940	162	162	162	157	65	40	669	352	209	209	209	205	205	Query Match Length
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Q19125	087181	Q9YW15	Q9xux6	Q9JKZ1	073635	Q9IAK5	Q9IAK6	Q91AK7	Q98882	Q99TK2	Q34216	Q9VPG2	Q9CGZ8	Q9R416	Q9S4S8	Q46325	Q9XD00	Q9XD01	IB
019125 caenorhabdi	087181 streptococc	Q9yw45 melanoplus	Q9xuk6 caenorhabdi	Q9jkzl meriones un	073635 fugu rubrip	-	٠.	_	Q98882 brachydanio	Q99tk2 staphylococ	•	_	lactoco	cowdria	Q9s4s8 cowdria rum	Q46325 cowdria rum	Q9xd00 ehrlichia c	Q9xd01 ehrlichia c	Description

ALIGNMENTS

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Q9XD00 PRELIMINARY; PRT; 205 AA. Q9XD00; Q9XD00; Q1-NOV-1999 (TremBLrel. 12, Created) Q1-NOV-1999 (TremBLrel. 12, Last sequence update) Q1-JUN-2001 (TremBLrel. 17, Last annotation update) MAJOR ANTIGENIC PROTEIN 2 HOMOLOG.	2	1 MKFLVNVALVENVVYISYIY 20 : :: ::	Query Match 50.9%; Score 55; DB 2; Length 205; Best Local Similarity 40.0%; Prod. No. 3.4; Matches 8; Conservative 7; Mismatches 5; Indels 0; Gaps	InterPro; IPR003782; SCO1_SenC. Pfam; PF02630; SCO1-SenC; 1. SEQUENCE 205 AA; 23169 MW; 756B50A3304C13CB CRC64;		BOWLE M.V., REDDY G.K., Semu S.M., Manan S.M., Barbet A.F.; "Potential Value of Major Antigenic Protein 2 for Serological Diagnosis of Heartwater and Related Ehrlichial Infections.":		NCBI_TaxID=944;	bacteria; al	1 2 HC	12, 17,	Q9XD01; 01-NOV-1999 (TrEMBLrel. 12, Created)	Q9XD01 PRELIMINARY; PRT; 205 AA.	TUT 1

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Query Match
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STRAIN-ARANSAS;
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Bowle M.V., Reddy G.R., Semu S.M., Mahan S.M., Barbet A.F.;
Bowle M.V., Reddy G.R., Semu S.M., Mahan S.M., Barbet A.F.;
Bowle M.V., Reddy G.R., Semu S.M., Mahan S.M., Barbet A.F.;
Bowle M.V., Reddy G.R., Semu S.M., Mahan S.M., Barbet A.F.;
Piagnosis of Heartwater and Related Ehrlichial Infections.";
Clin. Diagn. Lab. Immunol. 0:0-0(1999).
EMBL, AFI1731; AAD40620.1;
InterPro; IPR003782; SC01_SenC.
Pfam; PF02630; SC01-SenC; 1.
SEQUENCE 205 AA; 23142 MW; 561DC264B6EC9736 CRC64;
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SEQUENCE
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MEDLINE=95005467; PubMed=7921263;
Mahan S.M., McGuire T.C., Semu S.M., B
Rurangirwa F.R., Barbet A.F.;
"Molecular cloning of a gene encoding
of Cowdria ruminantlum";
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EMBL: L07385; AAA50280.1;
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Bacteria; Proteobacteria; alpha subdivision;
Rickettslaceae; Ehrlichieae; Cowdria.
NCBI_TaxID-779;
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Bacteria; Proteobacteria; alpha subdivision; Rickettsiales;
Rickettsiaceae; Ehrlichieae; Ehrlichia.
NCBI_TaxID=945;
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Pred. No. 8.7;
8; Mismatches
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for Serological
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10 984 S8
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Best Local S
Matches 7
                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 7
Q9CGZ8;
Q9CGZ8;
01-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q9R416;
Q9R416;
Q1-MAY-2000 (
Q1-MAY-2000 (
Q1-JUN-2001 (
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Q9S4S8;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Clin. Diagn. Lab. Immunol. 0:0-0(1999).
EMBL; AF117729; AAD40618.1; -.
EMBL; AF117728; AAD40617.1; -.
InterPro; IPR003782; SCO1_SenC.
Pfam; PF02630; SCO1-SenC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-UM BANEIN, AND PALM RIVER;
BOWHE M.V., Reddy G.R., Semu S.M., Mahan S.M.,
"Potential Value of Major Antigenic Protein 2 f
Diagnosis of Heartwater and Related Ehrlichial
Clin. Diagn. Lab. Immunol. 0:0-0(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bowie M.V., Reddy G.R., Semu S.M., Mahan S.M., "Potential Value of Major Antigenic Protein 2 f Diagnosis of Heartwater and Related Ehrlichial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; alprickettsiaceae; Ehrlichieae; Rickettsiaceae; Ehrlichieae; RCBI_TaxID=779;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rickettsiaceae;
NCBI_TaxID=779;
[1]
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Rickettsiaceae; Ehrlichieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Cowdria ruminantium
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cowdria ruminantium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE
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                                                                                                                                                                                                                                                                                                                   Similarity
7; Conser
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7; Conser
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1 (TrEMBLrel. 17, I
SENIC PROTEIN 2.
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209 AA; 23504 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      209 AA;
                                                                                                                                                                                                                                                                                                                      Conservative
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                                                         PRELIMINARY;
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AA; 23562 MW;
                                                                                                                                                                                                                                                                                                                                         48.1%;
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ae; Cowdria.
                                                                                                                                                                                                      27
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Last sequence up
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Pred.
                                                                                                                                                                                                                                                                                                                                                   Score 52;
Pred. No.
                                                            PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1C3699C5DE718ABB CRC64;
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DB 3.7;

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Length 209 Indels

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Gaps

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, Barbet A.F.; for Serological l Infections.";

RESULT Q46325 AC Q4 AC A

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Matches

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(TrEMBLrel.

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Rickettsiales;

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Matches

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RESULT
Q9VG2
ID VG2
AC Q9
AC Q
      RX MEDLINE-20196005; PubMed-10731132;

RA Adams M.D., Gelniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Adams M.D., Celniker S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Brandon R.C., Rogers M., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,

RA Cherry J.M., Cawley S., Dahlke C., Bavenport L.B., Davies P.,

RA Durbin K.J., Evangelista C.C., Ferraz C., Ferriera S., Dunkov B.C., Dunn P.,

RA Godson K., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,

RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan M., Glasser K.,

RA Haris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Haris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,

RA Haris N.L., Harvey D., Helman T.J., Wei M.-H., Ibegwam C.,

RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Haris N.C., Brottei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA McDull S.M., Mathei B., McIntosh T.C., McLeod M.P., McPherson D.,

RA McDulla N.V., Mobarry C., Morris J., Melson D.L.,
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Best Local S
Matches 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Drosophila melanogaster (Fruit fly)
Eukaryota; Metazoa; Arthropoda; Traa
Pterygota; Neoptera; Endopterygota;
Ephydroidea; Drosophilidae; Drosoph
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01-JUN-2001
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01-MAY-2000
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EMBL; AE006329; AAK05042.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-IL1403;
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Bacteria; Firmicutes; Bacillus/Clostridium group; Streptococcaceae;
Lactococcus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                lactis."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       UNKNOWN PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-JUN-2001 (TrEMBLrel. 17, 01-JUN-2001 (TrEMBLrel. 17,
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Moy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Last annotation updat
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Last annotation update)
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Pred. No. 22;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E4364E18CB252C09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tracheata; Hexapoda; Insecta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
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RESULT Q99TK2 ID Q9 AC Q9 DT 01

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Q99TK2; Q99TK2; 01-JUN-2001 01-JUN-2001

(TrEMBLrel. 17, (TrEMBLrel. 17,

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RRA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RRA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
Syirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA Yeng X.H., Zhong F.N., Zhong W., Zhong W., Zhou S., Zhu S., Zh
                                                                                                                                                                                     Query Match
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Best Local :
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01-NOV-1996
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                    Mitochondrion.
NON_TER
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EMBL; X75676; CAA53373.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-SR2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Candida parapsilosis (Yeast). Mitochondrion.
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InterPro; IPR002027; Amino_acid_permease.
Pfam; PF00324; aa_permeases; 1.
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LAFVISLLLVFFITYFVYIF
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8; Conserv
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a H.;
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                                                                                                                  Score 48; DB 8
Pred. No. 7.4;
7; Mismatches
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2 (FRAGMENT).
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Pred. No. 60;
7; Mismatches
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Best Loc
Matches
                                                                                                                                                Query Match 43.5%;
Best Local Similarity 41.2%;
Matches 7; Conservative
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KUTOGA M., Ohta T., Uchiyama I., Baba T., Yuzawa H., Kobayashi I.,

Gui L., Oquchi A., Aoki K.I., Nagai Y., Lian J., Ito T., Kanamori M.,

Matsumaru H., Maruyama A., Murakami H., Hosoyama A., Mizutani-Qi Y.,

Takahashi N.K., Sawano T., Tooue R.I., Kaito C., Sekimizu K.,

Takahashi N.K., Sawano T., Tooue R.I., Kaito C., Sekimizu K.,

Hirakawa H., Kuhara S., Goto S., Yabuzaki J., Kanbisa M.,

Yamashita A., Oshima K., Furuya K., Yoshimo C., Shiba T., Hattori M.,

Ogasawara N., Hayashi H., Hiramatsu K.;

Whole genome sequencing of meticillin-resistant Staphylococcus

aureus ".

Lancet 357:1225-1240(2001).

EMBL, A0003134; BAB42742.];

Lancet 357:1225-1240(2001).
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HYPOTHETICAL PROTEIN SAL477.
SAL477:
SAL477:
Staphylococcus aureus subsp. aureus N315.
Bacieria; Firmicutes; Bacillus/Clostridium group;
Bacieria; Firmicutes; Bacillus/Clostridium group;
Bacieria; Firmicutes; Bacillus/Clostridium group;
Bacieria; Firmicutes; Bacillus/Staphylococcus.
MCBI_TaxID-158879;
                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Acclinopterygli; Neopterygli; Teleostel; Euteleostel; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Hypotherical protein; Complete proteome.
SEQUENCE 65 AA; 7517 MW; D875CCB2A08C70E8 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Webth F. Nadler W., Korsching S.;

"Wested expression domains for odorant receptors in zebrafish
Lfactory epithelium.";

Proc. Natl. Acad. Sci. U.S.A. 93:13321-13326(1996).

END. U72693; AAB18866; U.S.A. 93:13321-13326(1996).

END. CEBRES 190415-190; Zozl.

InterProc. IPRO0276; GCP_Rhodpsn.

PROSITE: PSS0262; G_PROTEIN_RECEP_F1_2; 1.
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77 LIGLLITFILILISYVY 93
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157 AA;
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17656 MW;
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                                                                                                                                           Score 47; DB 13; Length 157; Pred. No. 32; 6; Mismatches 4; Indels
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Pred. No.
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Rouguler'S, Blancher A., Glorgi D.;
"The olfactory receptor gene repertoire in primates and mouse: Bridence for reduction of the functional fraction in primates.";
Proc. Natl. Acad. Sci. U. S., 97:2870-2874(2000).
[InterPro. PREMOO275; GPCR_Rhoman.
                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-20183981: pubMed=10706615;
MEDLINE-20183981: pubMed=10706615;
ROUQUIET S., Blancher A., Glorgi D.;
The olfactory receptor gene repertoine in primates and mouse:
Evidence for reduction of the functional fraction in primates.";
Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000).
EMBL; AF179845; AF404010.1;
EMBL; AF179845; AF40410.1;
EMBL; AF179845; AF404010.1;
EMBL; AF179845; AF40410.1;
EMBL; AF179845; AF404010.1;
EMBL; AF479845; AF479845;
EMBL; EM
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Bukarytta: Metazoa (Chrontata; Vertebrata; Euteleostomi,
Actinopterygii; Neopterygii; Teleostai; Euteleostei; Ostariophysi;
Oppiniformes; Cyprinidae; Rasborinae; Danio.
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091AK6;
01-CCT-2000 (TremBLrel. 15, Cro
01-CCT-2000 (TremBLrel. 15, Las
01-JUN-2001 (TremBLrel. 17, Las
01-JUN-2001 (FRAGMENT)).
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Eukaryota: Methazos: Chordeta: Cranista: Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Buteleostei; Ostariophysi;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
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091AK7;
01-CCT-2000 (TremBLrel. 15, Cr
01-CCT-2000 (TremBLrel. 15, Las
01-UN-2001 (TremBLrel. 17, Las
01-MN-2001 (TremBLrel. 17, Las
01-MN-2001 (TremBLRel. 17, Las
                                                                                                                                                   Pfam; PF00001; 7t
PROSITE; PS50262;
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PE; PS50262;
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7: Conservative
1
162 AA;
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162
162 AA;
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52; G_PROTEIN_RECEP_F1_2;
1
162
18122 MW;
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18156 MW;
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Pred. No. 33;
6; Mismatches
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     7877B0A46EF2B949 CRC64;
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Query Match Best Local Similarity

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Conservative

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Best Local S
Matches 7
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073635; PRELIMINARY:
01-AUG-1998 (TrembLrel: 07, L
01-JUN-2001 (TrembLrel: 17, L
CALCIUM2+ SENSING RECEPTOR.
                                                       Proc.
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NON_TER
SEQUENCE
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SEQUENCE FROM N.A.
MEDLINE=20183981; PubMed=10706615;
MEDLINE=20183981; PubMed=10706615;
MEDLINE=20183981; PubMed=10706615;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Evidence for reduction of the functional fraction in primates. Proc. Natl. Acad. Sci. U.S.A. 97:2870-2874(2000). EMBL: AF179845; AAF40411.1; -. Interpre. Terroconcer.
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Ł
Actinopterygii; Neopterygii; Teleostei; Euteleostei;
Cypriniformes; Cyprinidae; Rasborinae; Danio.
NCBI_TaxID=7955;
    InterPro;
InterPro;
                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE-922678B; PubMed-9560249;

NAITO T., Saito Y., Yamamoto J., Nozaki Y., Tomura K.,

Nakanishi S., Brenner S.;
                                                                                                                                                                                                                                                       Fugur rubripes (Japanese pufferfish) (Takifugu rubripes).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei
Acanthomorpha; Acanthopterygii; Percymorpha; Tetraodontiformes;
Tetraodontidae; Takifugu.
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                                       InterPro;
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                                                                                                                "Putative pheromone receptors related to
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Natl. Acad. Sci. U.S.A. 95:5178-5181(1998).
AB008857; BAA26122.1; -.
Pro; IPR000337; GPCR_Mgr.
Pro; IPR000651; RASGEFN.
Pro; IPR001828; ANF_receptor.
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7; Conservative
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18130 MW;
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WONNEDETGET K., SCOTIELD M.A., Wangemann P.;
"Evidence for a calcium sensing receptor in the
cells of the spiral modiolar artery.";
Submitted (JAN-2000) to the EMBL/GenBank/DDBJ da
EMBL; AF221064; AAF37826.1;
PROSITE; PS09981; G-PROTEIN_RECEP_F3_3; 1.
PROSITE; PS09259; G-PROTEIN_RECEP_F3_4; 1.
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NCBI_TaxID=10047;
[1]
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SEQUENCE
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Pfam; PF01094; ANF_receptor; 1.
PRINTS; PR00248; GPCRMGR.
PROSITE; PS00979; G_PROTEIN_RECEP_F3_1; 1.
PROSITE; PS0259; G_PROTEIN_RECEP_F3_4; 1.
SEQUENCE 940 AA; 105813 MM; 06DAB7803B6878B3 CRC64;
                                                                                                                                                                                                                                                                                                                                               Meriones ungulculatus (Mongolian jird).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammmalia; Eutheria; Rodentia; Sciurognathi; Muridae;
                                                                                                                                                                                                                                                                                                                                                                                                           01-0CT-2000 (TrEMBLrel. 15, Created)
01-0CT-2000 (TrEMBLrel. 15, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation updat
CALCIUM-SENSING RECEPTOR (FRAGMENT).
                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
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Similarity
9; Conser
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                 Score
Pred
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Pred. No. 2e+02;
5; Mismatches
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54;
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; Gerbillinae;
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